

**FIGURE 1**

CGGACGCGTGGGTGCGAGGCCGAAGGTGACCGGGGACCGAGCATTTTCAGATCTGCTCGGTAGA  
CCTGGTGCACCACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG  
GTTTTCCACCCAGCTTTCACCAAGGCCTCCCCTGTTGTGAAGAATTCCATCACGAAGAATCA  
ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA  
GAACTGGCCAAGAACTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAAATATTTAAAATT  
GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA  
CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT  
ATGTCAAGGATAGAATTCATTCACCTATATGTACTTAGCAGGGAGTATTGGTTTAAACAGCT  
TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACTTCATGATGAGAGGCTCTTG  
GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC  
CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT  
GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC  
AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAAAGTTTCTGA  
ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG  
TTTCTTCCACCTACCACCGTGGCTGGTGGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT  
AGTTCCTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT  
CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACCTCGATGCTGAGTATCTACATGGAT  
ACATTAAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**TC**  
**A**AGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTAATGGGGCAGATATGC  
ATTAAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA  
TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT  
AATCCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAAATGTT  
TTGGTGAATGTGAAAATAAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA  
TTTAGTAGGITEACTGAGTAACTAAAATTTAGCAAACCTGTGTTTGCATATTTTTTTGGAGT  
GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG  
GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA  
GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAAACAAGTGGTCATTGTTACATTCATTT  
GCTGAACTTAACAAAACCTGTTTCATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG  
CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC  
ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA  
ATAACTTTAAAACATTTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG  
AATACAAACAGTATACTCATG

094192 082804  
102230 266466

**FIGURE 2**

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL  
KEAALEPSMEKIFKIDQMGRWVAVAGGAAGVGLGALCYGLGLSNEIGAIEKAVIWPQYVKDRI  
HSTMYLAGSIGLTALSAIAISRTPVLMNFMMRGWSVTIGVTFAAMVGAGMLVRSIPYDQSP  
GPKHLAWLLHSGVMGAVVAPLTIILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL  
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFSMFLLYDTQKVIKRAEVSPMYGV  
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

094199.08204  
T0220.256450

**FIGURE 3**

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCCCGTCTCCGCCTTCTGCAT  
CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCCGCGGAGCCGGCCGCGTCTGTGAGGG  
GGTCGGCACGGGGAGTCGGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTCAAG**ATG**TCGG  
ACATCGGAGACTGGTTCAGGAGCATCCCCGGCATCACGCGCTATTGGTTCGCCGCCACCGTC  
GCCGTGCCCTTGGTCGGCAAACCTCGGCCTCATCAGCCCCGGCCTACCTCTTCCTCTGGCCCCGA  
AGCCTTCCTTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGG  
GTCCAGGAACCTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGCGA  
CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG  
GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCCTCTGATCA  
TGTCAGTACTTTATGTCTGGGCCCAGCTGAACAGAGACATGATTGTATCATTTTTGGTTTTGGA  
ACACGATTTAAGGCCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG  
CTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTTCCCTAATGTTCA  
GATACCCAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGG  
CTGCCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC  
TGCTGATCAGAATGGCGGAGGCGGGAGACACAACCTGGGGCCAGGGCTTTCGACTTGGAGACC  
AG**TGA**AGGGGCGGCCTCGGGCAGCCGCTCCTCTCAAGCCACATTTCCCTCCAGTGCTGGGTG  
CACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC  
AGTACGAGACAAAGTTTCTTAAATCCCCGAAGAAAAATATAAGTGTTCACAAAGTTTCACGAT  
TCTCATTCAAGTCCTTACTGCTGTGAAGAACAATAACCAACTGTGCAAAATTGCAAACTGAC  
TACATTTTTTGGTGTCTTCTCTTCTCCCCCTTTCCGTCTGAATAATGGGTTTTAGCGGGTCTT  
AATCTGCTGGCATTGAGCTGGGGCTGGGTCACCAAACCCTTCCCAAAGGACCTTATCTCTT  
TCTTGACACATGCCTCTCTCCCACTTTTCCCAACCCCCACATTTGCAACTAGAAAAAGTTG  
CCCATAAAATTGCTCTGCCCTTGACAGGTCTGTATTTATTGACTTTTGCCAAGGCTGGTC  
ACAACAATCATATTCACGTTATTTTCCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG  
AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATTGCTTCGACTGACATCCGTTGTT  
AACCCTTTGCCACTCTTCAGATATTTTTTATAAAAAAAGTACCACTGAGTTCATGAGGGCCA  
CAGATTGGTTATTAATGAGATACGAGGGTTGGTGTGGGTGTTTGTTCCTGAGCTAAGTGA  
TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTAAACCATGGGGGATGCACCCC  
TTTGCCTTTTGGTGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGCTTGTCTTGTGT  
TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTG  
ATTCCCATTTCAATCTCATTCTGGATATGTGTTTATTGAGTAAAGGAGGAGAGACCCTCATA  
CGCTATTTAAATGTCACCTTTTTTGCCTATCCCCCGTTTTTTGGTTCATGTTTCAATTAATTGT  
GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA  
AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGAGGGTGTGTTA  
TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTTT  
TCGTAGGTGGGCTTTTCCCTATCAGAGCTTGGCTCATAACCAAATAAAGTTTTTTGAAGGCCA  
TGGCTTTTTCACACAGTTATTTTATTTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT  
ATTGAGTGGCTGTCACACTTTGAGGCAACTAAAAAGGCTTCAAACGTTTTGATCAGTTTCTT  
TTCAGGAAACATTGTGCTCTAACAGTATGACTATTCTTTCCCCCACTCTTAAACAGTGTGAT  
GTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTTGTGTG  
TACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGAGAGTCTGAACCTTAACTGTCA  
TGTTTTGTGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAATTTTAGAGGCCATTACT  
CCAATTATGTTGCACGTACACTATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATA  
TTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGTAACCTCTTACCAGTCAGCTGCCTGCGAG  
CAGTCATTTTTTCCCTAAAGGTTTACAAGTATTTAGAAGTTTTCAGTTTCAGGGCAAAATGTTT  
ATGAAGTTATTCCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGATT  
ATGTTTCTGGAATAATTTTACCAAACAAGCTATTTGAGTTTTGACTTGACAAGGCAAAACA  
TGACAGTGGATTCTCTTTACAAATGGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCC  
TTTTTGTAACATAATCCTTTTTTATTGGTAAAAATTGTAAATTAAATGTGCAACTTG

**FIGURE 4**

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGLISPAYLFLWPEAFLYRFQIWRPITATFYF  
PVGPGTGFLYLVNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWCIVITGLAMDMQLLMIP  
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL  
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRL  
GDQ

**Transmembrane domain:**

amino acids 98-116, 152-172

**N-myristoylation site.**

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

**Glycosaminoglycan attachment site.**

amino acids 218-222



**FIGURE 5**

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG  
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT  
 CCTTGTGGCCCAAAGGCCTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTTGCC  
 CCTTTGGGGCGGG**ATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG  
 CGGGGTTCCCTGCGAGGCCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT  
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT  
 GGCCTGTGTTCCCCTTGTTTTTGGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC  
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT  
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC  
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA  
 AAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTACCT  
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT  
 GAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA  
 AACAGTTATCAGAGGCTAAAACAGAAGAGCCACAGTGCATTCCAGTGAAGCTGCAATAATG  
 AATAATTTCCAAGGGGATGGTGAACATTTTGCACACCCACCCTCAGAAGTTAAATGCATTT  
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAACTTCCTCCCTCC  
 CACAAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC  
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA  
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG  
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG  
 CAAACATTACTAAAGAGGAGATTGCTTGCAAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**  
**A**TAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC  
 CTTACACTG

**FIGURE 6**

MAAEEEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPEPVILVACVP  
LVFDDEEESKLTYTEIHQEYKELVEKLLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP  
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGLPDCLTDGSDVVSLEHEEMKILREVL  
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS  
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS  
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRLLAEKLKEEVINK

**N-glycosylation sites.**

amino acids 224-228, 246-250, 285-289

**N-myristoylation site.**

amino acids 273-279

**Amidation site.**

amino acids 252-256

**Cytosolic fatty-acid binding proteins.**

amino acids 78-108

**FIGURE 7**

GGGCACAGCACATGTGAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT  
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA  
TTAATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAG  
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC  
AGAAAAACATTGAAATGCAGCTGCAAGCCATTCTGAATAATTCAAGAGAGAAATGGTGTATTA  
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAT  
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA

T0220"255T1550

**FIGURE 8**

GCGTGGTTTTTGTTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTG  
 TAGCTTCTCCACGTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG  
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTA AAAAAC  
 AGTGGAATGGAAAAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATAC  
 ATTCCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT  
 CTGCCAATGAAGAAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTG  
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCAATTCTGTGTTATAAAGAAAGATCATCAAAGTAG  
 AAATTTGAAATATGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCT  
 TTCTTTATTTCTGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATG  
 GCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGGATAGTGCTGAA  
 GAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCT  
 TGACTGCCGGGACTAAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTCATCACGATGCC  
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG  
 TACAGCAAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC  
 ACATCCGTCTTGGCATGGGCCATGTTCTTATTATAGTCCAGTGTTTTATTTCTTCAATGGCT  
 AATATCTATAATGAAAAGATACTGAAGGAGGGGAACCAGCTCACTGAAAGCATCTTCATACA  
 GAACAGCAAACCTCTATTTCTTTGGCATTCTGTTTAATGGGCTGACTCTGGGCCTTCAGAGGA  
 GTAACCGTGATCAGATTAAGAACTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC  
 CTTATTTTTGTAACTGCATTCCAGGGCCTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA  
 CATGTTCCATGTCTTGATGGCCCAGGTTACCACTGTCATTATCACAAACAGTGTCTGTCTGCTG  
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGGAAGCCCCATCAGTCCTTCTCTCTATA  
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGAATACGCACCTAGGCAAGAAAGGATCCG  
 AGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTTA  
 CCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA  
 GCTCTCTTGAACCTTATTTTTCACATTTTCAGTGTTTGTAATATTTATCTTTTCACTTTGATA  
 AACCAGAAATGTTTCTAAATCCTAATATTCTTTGCATATATCTAGCTACTCCCTAAATGGTT  
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATTCTAAAGAACTGATACAGGAGTAACA  
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT  
 TTTCTTGGCCCTTCAAGCTTCCAAAAAACTTGTAATAATCATGTTAGCTATAGCTTGTATAT  
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGT  
 CTTCCCTTTTTTAACATTATAAAAGCTAGGTTGTCTCTTGAATTTTGAGGCCCTAGAGATAGT  
 CATTTTGCAAGTAAAGAGCAACGGGACCCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC  
 CTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGTCTAAATATTTTGCTGAAGAAGCAGT  
 TTCTCAGACACAACATCTCAGAAATTTAATTTTTTAGAAATTCATGGGAAATTGGATTTTTGT  
 AATAATCTTTTGATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTACCACTTGTATTTTA  
 AGTCATTTAAACAAGCCACGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGAT  
 GTCATTACTCCTGAATTATTACATTTTGGAAGAATAAGAGGGCATTTTTATTTTATTAGTTACT  
 AATTCAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAAATGCTGGCTTCAGAATCATAC  
 CAGATTGTGCTAGTGAAGCTGATGCCTAGGAACCTTTTAAAGGGATCCTTTCAAAGGATCACTT  
 AGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAAAGACC  
 AGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAGTGCATGGTATTTTTTCATG  
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAA  
 AAATTAGCAAACAAAAGTGACTTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGG  
 CTTTAACTGGCAGGCCTGTATGTTTACAGACTACCATACTGTAAATATGAGCTTTATGGTGT  
 CATTTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA  
 AGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAATTG  
 GTGGAAATTTGTAATTAAATAATTATTAAACCT

## **FIGURE 9**

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSSELVK  
LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV  
IFS NFSIIT TALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF  
SPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI  
YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI  
FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI  
YNASKPQVPEYAPRQERIRDL SGNLWERSSSGDGEELERLTKPKSDESDETF

### **Transmembrane domains:**

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,  
298-318, 328-368

### **N-glycosylation sites.**

amino acids 128-132, 204-208, 218-222, 374-378

### **Glycosaminoglycan attachment site.**

amino acids 402-406

### **N-myristoylation sites.**

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

**FIGURE 10**

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG  
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC  
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG  
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAACAGTGGAATGGAA  
AAACAGTGCTGTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCCCTGCTAGG  
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG  
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT  
TTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA  
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCCCTGCCTTTCTTTATTTCC  
TGGATAACTTGATTGTCTTCTATGTCCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTC  
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTCAAGGATAGTGCTGAAGAGGCGTCTAAA  
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA  
CTAAAACTTTA

**FIGURE 11**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC  
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCCTGCGGGGCAGAGGAGCAT  
 CCCGTCTACCAGGTCCCAAGCGGCGTGGCCCGCGGGTTCATGGCCAAAGGAGAAGGCGCCGAG  
 AGCGGCTCCGCGGCGGGGCTGCTACCCACCAGCATCCTCCAAAGCACTGAACGCCCCGGCCCA  
 GGTGAAGAAAGAACCAGAAAAAGAAGAAACAACAGTTGTCTGTTTGCAACAAGCTTTGCTATG  
 CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC  
 CTATTGG**ATG**TGGCTCAGGTGGGCCCTTTCTCTGCCTCCATCATCCTGTTTGTGGGCCGAGC  
 CTGGGATGCCATCACAGACCCCCCTGGTGGGCCTCTGCATCAGCAAATCCCCCTGGACCTGCC  
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCCCTGGCCGTCAATTGCCTACTTCCTC  
 ATCTGGTTCGTGCCCCACTTCCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT  
 CTTTGAAACAATGGTCACGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA  
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGCTGGGCAC  
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCTTGTTTCCAGG  
 ACTTCAATAGCTCTACAGTAGCTTCACAAAGTGCCAACCATAACATGGCACCACCTTCACAC  
 AGGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCAATTGTCTGTATCTATATAATCTG  
 TGCTGTATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTG  
 AGCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATAACATCAAACCTT  
 ATTACTGGCTTCCTCTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACCTTTGTCTTGTT  
 TTGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCT  
 CGGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT  
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA  
 CCTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC  
 TACCCTGGTCCATGCTGCCTGATGTCAATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT  
 GGAACCGAGCCCATCTTCTTCTCCTTCTATGTCTTCTTCACCAAGTTTGCCTCTGGAGTGTG  
 ACTGGGCATTTCTACCCTCAGTCTGGACTTTGCAGGGTACCAGACCCGTGGCTGCTCGCAGC  
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG  
 CTGGGCCTGCTGCTCTTCAAATGTACCCCATTTGATGAGGAGAGGCGGCGGCAGAATAAGAA  
 GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG  
 AGCTGGCTAGCATCCTC**TAG**GGCCCCGCCACGTTGCCCCGAAGCCACCATGCAGAAGGCCACAG  
 AAGGGATCAGGACCTGTCTGCCGGCTTGCTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA  
 CTGAAGACTCAAGGAGGTGGCCCAGGACACTTGCTGTGCTCACTGTGGGGCCGGCTGCTCTG  
 TGGCCTCCTGCCTCCCCTCTGCCTGCCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA  
 TGCCAAGGACTGATCGGGCCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC  
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTGTATGTATATGTCTGTGAGCTA  
 TTAATGTTATTAATTTTCATAAAAGCTGGAAAGC

**FIGURE 12**

MWLRWALSLPPSSCLWAEPGMPSQTPWWASASANPPGPAWVALCPGSSSPRPWPSLPTSSSG  
SCPTSHTARPIGTGCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL  
GTAIQQQIVGQADTPCFQDFNSSTVASQSANHHTGTTSHRETQKAYLLAAGVIVCIYIICAV  
ILILGVREQREPYEAAQQSEPIAYFRGLRLVMSHGPIYIKLITGFLFTSLAFMLVEGNFVLFCT  
YTLGFRNEFQNLLLAIMLSATLTIPWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI  
ITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYVFFTKFASGVSLG  
ISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLFKMYPIDEERRRQNKAL  
QALRDEASSSGCSETDSTELASIL

FO220"256TH60



**FIGURE 13**

GGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT  
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA  
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATAACATCAAACCTTA  
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT  
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC  
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG  
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC  
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT  
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG  
GAACCGAGCCCAT

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**FIGURE 14**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT  
ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAACAGAAAACCTGTTAGAA**ATGT**  
GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT  
TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT  
CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG  
CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA  
GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGTACTTGGAATACTGAGTTGTTTAGG  
ACTTTCTATTGTGGCAAACCTTCCAGAAAACAACCCTTTTTGCTGCACATGTAAGTGGAGCTG  
TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCCTACCAAATG  
CAGCCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG  
AGTAAGTGCACTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG  
ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTATGTGCTTCACATGATCACT  
ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTTCTGACTTACATTCGTGA  
TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAACCCCTCTATGACACTG  
CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATT**TGAT**GAAAGGAT  
AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAGTTGCTTA  
TTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA  
ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA  
TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

**FIGURE 15**

MWWFQQGLSFLPSALVIWTSAAFI~~F~~SYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI  
AAVLCIATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSG  
AVLTFGMGSLYMFVQTILSYQM~~Q~~PKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFG  
TDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT~~Y~~IRDFQKISLRVEANLHGLTLYD  
TAPCPINNERTRLLSRDI

**FIGURE 16**

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT  
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA  
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTTGAAGCAGT  
TACCAAGAATCTTCAACCCTTTCCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA  
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA  
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT  
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT  
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

**FIGURE 17**

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG  
 CCGGGGTGCGGAGCCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC  
 CTTGCGCTTGTACTTGCTGTGACGCGACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGG  
 AGGCTGGAGGCAGGTGCTGTGGTTCCCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG  
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCCCTGCTCTTCTGCGGCGCCTA  
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT  
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC  
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCCTGATAAAGT  
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT  
 TGAGACTTTTCCCCATGACACCAAAGTGGTTCTTGAACCTCTCGGCCCCAATTCTGAACATT  
 CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAATTTCTATCTGTGT  
 GCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTG  
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCTCATTAAAAAATTT  
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA  
 CACATTCATCTGGATTTTCTGTTTGCCACATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA  
 TGTGGTCTCTAAAGCCCCCTCATTGTTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG  
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT  
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGT  
 GGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC  
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAT  
 ACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCCAGCTACTCGGGAGGCTGAGGC  
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT  
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

**FIGURE 18**

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYR  
KEHQAYVFLLFCGAYLYKQGFAIPGSSFLNVLGALFGPWLGLLLCCVLTSVGATCCYLLSS  
IFGKQLVVSYPDPKVALLQRKVEENRNSLFFLLFLRLFPMTPNWFLNLSAPILNIPIVQFF  
FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ  
LNETSTANHIHSRKDT

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 101-123, 189-211

**N-glycosylation sites.**

amino acids 172-176, 250-254

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 240-244, 261-265

**N-myristoylation site.**

amino acids 13-19, 104-110, 115-121, 204-210

**Amidation site.**

amino acids 27-31

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 4-15

**Protein splicing proteins.**

amino acids 25-31

**Sugar transport proteins.**

amino acids 162-172

**FIGURE 19**

CCGAGGCGGGAGGAGCCCCGAGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT  
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA  
 TAGGAAAATAACTTGGGATTTTATATTGGAAGAC**ATG**GATCTTGCTGCCAACGAGATCAGCA  
 TTTATGACAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG  
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC  
 CCCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT  
 TGCTCACTGCCTACTTTGTGATTCAACCTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCT  
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA  
 GAAGTACATGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCCTTTC  
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTGCC  
 AACTGCACTGGCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA  
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCCTGTTGGAGGAAGAGATTC  
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG  
 TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA  
 CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATG  
 CCTCTTTAAACAAGTGCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG  
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA  
 GTGCCGAAGACATTGTCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG  
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT  
 GGAACCGCTTTCTCAGAACTG**TAG**GAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA  
 AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAAA

**FIGURE 20**

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVY  
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPL  
HGGDEDRPFPDFDPWWTNDCEQNESEPI PANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT  
GKPLLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFFPYPWRRPLNRSQMLRELFV  
FTHLPFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRCQSVAMP  
IEPGDIGYVDTHWKVYVIARGVQPLVICDGTAFSEL

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**FIGURE 21**

CCACGGTGTCCGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCGAGGGGCG  
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTTCAGTTGTGATC  
AAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT  
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTCAGAGACTGTTG  
ATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC  
AGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT  
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC  
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

**FIGURE 22**

CCCACGCGTCCGCCCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG  
 CAGGGTCCCCACTTGACAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG  
 CCACTGGTGCGCACGCTGCTAGACCGTGCCATATGAGCCGCTGGGGCTGCAGTGGGGACTGCC  
 CTCCCTGCCACCCACCAATGGCAGCCCCACCTTCTTTGAAGACTTCCAGGCTTTTTTGTGCCA  
 CACCCGAATGGCGCCACTTTCATCGACAAACAGGTACAGCCAACC**ATG**TCCAGTTTCGAAATG  
 GACACGTATGCTAAGAGCCACGACCTTATGTTCAGGTTTCTGGAATGCCTGCTATGACATGCT  
 TATGAGCAGTGGGCAGCGGCCAGTGGGAGCGCGCCAGAGTCGTCGGGCTTCCAGGAGC  
 TGGTGCTGGAACCTGCGCAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGCTG  
 AAGCAGCAGGCAACGCAGCACTCCATGGCCCTGCTGCAGTGGGGGGCGCTGTGGCGCCAGCT  
 CGCCAGCCCATGTGGGGCTGGGCGCTGAGGGACACTCCCATCCCCCGCTGGAAACTGTCCA  
 GCGCCGAGACATATTACGCATGCGTCTGAAGCTGGTGCCCAACCATCACTTCGACCCCTCAC  
 CTGGAAGCCAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCCTGACACCCACCGAGGAGGC  
 CTCACTGCCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCCAGTTGCTGCAGG  
 AGGACCAGCTCGGCGAGGACGAGCTGGCTGAGCTGGAGACCCCGATGGAGGCAGCAGAACTG  
 GATGAGCAGCGTGAGAAGCTGGTGCTGTGCGCCGAGTGCCAGCTGGTGACGGTAGTGGCCGT  
 GGTCCCAGGGCTGCTGGAGGTACCCACACAGAATGTATACTTCTACGATGGCAGCACTGAGC  
 GCGTGGAACCGAGGAGGGCATCGGCTATGATTTCCGGCGCCCACTGGCCAGCTGCGTGAG  
 GTCCACCTGCGGCGTTTCAACCTGCGCGCTTACGACACTTGAAGCTCTTCTTTATCGATCAGG  
 CAACTACTTCTCAACTTCCCATGCAAGTTGGGACGACCCAGTCTCATCTCCTAGCCAGA  
 CTCCGAGACCCAGCCTGGCCCCATCCCACCCCATACCCAGGTACGGAACAGGTGTACTCG  
 TGGCTCCTGCGCCTACGGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCCCCAGGAGAT  
 GCTGCGTGCTCAGGCCTTACCCAGAAATGGGTACAGCGTGAGATATCCAACTTCGAGTACT  
 TGATGCAACTCAACACCATTTGCGGGGCGGACCTACAATGACCTGTCTCAGTACCCGTGTGTT  
 CCCTGGGTCCTGCAGGACTACGTGTCCCCAACCCCTGGACCTCAGCAACCCAGCCGTCTTCCG  
 GGACCTGTCTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCCAGCTCGTGAGGGAGAAGT  
 ATGAAAGCTTTGAGGACCCAGCAGGGACCATTTGACAAGTTCCACTATGGCACCCACTACTCC  
 AATGCAGCAGGCGTGATGCACTACCTCATCCGCGTGGAGCCCTTCACCTCCCTGCACGTCCA  
 GCTGCAAAGTGGCCGCTTTGACTGCTCCGACCGGCAGTTCCACTCGGTGGCGGCAGCCTGGC  
 AGGCAGCCCTGGAGAGCCCTGCCGATGTTGAAGGAGCTCATCCCGGAATTCTTCTACTTTTCT  
 GACTTCTTGAGAAACAGAACGGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT  
 AGGCGATGTGGTGCTACCCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCCGCC  
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC  
 TACAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTATTACTGCACCTATGA  
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGGAACGGAAGGCTCTGGAGGGCATT  
 TCAGCAACTTTGGGCAGACTCCCTGTGAGTGTGAAGGAGCCACATCCAACCTCGGCTCTCA  
 GCTGAGGAAGCAGCCCATCGCCTTGACGCGCTGGACACTAAGTCACTAGCATCTTCCAGCA  
 CCTGGACGAACTCAAGGCATTTCTTCGAGAGGTGACTGTGAGTGCCAGTGGGCTGCTGGGCA  
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTTCAGCTTCAGCAAAAGACCCC  
 ACCATGGGCAGCCACAAGACGCAGCGACTGTGAGTGGCCCGTGGGTGCCAGGCAGTGGTGT  
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAAGCTGCTATTACGCGGTGGCCACTGGG  
 ATGGCAGCCTGCGGGTGAAGTGCATACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC  
 CTTGATGTAGTAACCTGCCTTGCACTGGACACCTGTGGCATCTACCTCATCTCAGGCTCCCC  
 GGACACCACGTGCATGGTGTGGCGGCTCCTGCATCAGGGTGGTCTGTCACTAGGCCTGGCAC  
 CAAAGCCTGTGACGGTCTGTATGGGCATGGGGCTGCAGTGAAGTGTGTGGCCATCAGCACT  
 GAACTTGACATGGCTGTGTCTGGATCTGAGGATGGAAGTGTGATCATAACACTGTACGCCG  
 CGGACAGTTTGTAGCGGCACTACGGCCTCTGGGTGCCACATTTCCCTGGACCTATTTTCCACC  
 TGGCATTGGGGTCCGAAGGCCAGATTGTGGTACAGAGCTCAGCGTGGGAACGTCTGGGGCC  
 CAGGTACCTACTCCTTGACCTGTATTGAGTCAATGGGAAGTTGCGGGCTTCACTGCCCT  
 GGCAGAGCAGCCTACAGCCCTGACGGTGACAGAGGACTTTGTGTTGCTGGGCACCGCCAGT  
 GCGCCCTGCACATCCTCCAACATAACACACTGCTCCCGGCCGCGCCTCCCTTGCCCATGAAG  
 GTGGCCATCCGCAGCGTGGCCGTGACCAAGGAGCGCAGCCACGTGCTGGTGGGCTGGAGGA  
 TGGCAAGCTCATCGTGGTGGTTCGCGGGGCGAGCCCTCTGAGGTGCGCAGCAGCCAGTTCGCG  
 GGAAGCTGTGGCGTCTCCTCGCGGCGCATCTCCAGGTGTCCTCGGGAGAGACGGAATACAC  
 CCTACTGAGGCGCGCT**TGA**ACCTGGCCAGTCCGGCTGCTCGGGCCCCCGCCCCGGCAGGCCTG  
 GCCCGGGAGGCCCCCGCCAGAAAGTCGGCGGGAACACCCCGGGGTGGGCAGCCAGGGGGTGA  
 GCGGGGGCCACCCTGCCAGCTCAGGGATTGGCGGGCGATGTTACCCCTCAGGGATTGGCG  
 GGCGGAAGTCCCGCCCCCTCGCCGGCTGAGGGGCGGCCCTGAGGGCCAGCACTGGCGTCT

**FIGURE 23**

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL  
 RYTAVLKQQATQHSMALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN  
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALELETP  
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSTERVETEEGIGYDFRRP  
 LAQLREVHLRFRNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQPGPIPPHTQV  
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL  
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPAGTIDKFH  
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESPADVKELEIP  
 EFFYFPDFLENQNGFDLGCLQLTNEKVGDVLPWASSPEDFIQQHRQALESEYVSAHLHEW  
 IDLIFGYKQRGPAEEEEALNVFYCYTYEGAVDLDHVTDERERKALEGIIISNFGQTPCQLLKEP  
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF  
 SFSKDPTMGSHKTQRLLSGPWVPGSGVSGQALAVAPDGKLLFSGGHWGSLRVLTALPRGKLL  
 SQLSCHLDVVTCLALDTCGIYLIISGRDTCMVWRLLHQGGLSVGLAPKPVQVLYGHGAAVS  
 CVAISTELDMAVSGSEDGTVIIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA  
 WERPGAQVTYSLHLYSVNGKLRLASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA  
 PPLPMKVAIRSVAVTKERSHVLVGLEDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSS  
 GETEYNPTAR

**N-glycosylation site.**

amino acids 677-681

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 985-989

**Tyrosine kinase phosphorylation site.**

amino acids 56-65, 367-376, 543-551

**N-myristoylation site.**

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,  
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,  
 873-879, 912-918, 954-960

**FIGURE 24**

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC  
CACGGCCCACCTTGTGAACTCCTCGTGCCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT  
CCAAAGGCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCCTGGGGCTCTTC  
TGGACCCTTAACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTT  
CTACTGGGCCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC  
GCACACTCCGTTACCACACTGGGTCATTGGCATTGAGGCCCTCATCCTGACCCTTGTGCAG  
ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC  
CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC  
TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA  
AATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGTCGTCCTGGACAAAGTCACAGA  
CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTCGGAGGCGTGGGGGTCTGTCTTCTTTT  
TTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAGACTTTAAGAGCCCCCACCTCAACTATTAC  
TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCATCGCCAGCGGCTTCTTCAGCGT  
TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG  
GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC  
GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGGCCCTGATCCAGGACTGC  
ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT  
AAAAAAGGTTTTAGGCCAGGCGCCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG  
AGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC  
GTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCATCCCAGCTAC  
TCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA  
TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAA  
AAAGATTTTATTAAAGATATTTTGTAACTC

**FIGURE 25**

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLF  
WTLNWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ  
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK  
NAFMLLMRNIVRVVLDKVTDLLLFFGKLLVGGVGVLSTFFFSGRIPGLGKDFKSPHLNYY  
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYSKSLKILGKKN  
EAPPDNKKRKK

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**FIGURE 26**

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGT  
 GGCT**ATG**TTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC  
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTTC  
 CAGTGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC  
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG  
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGG  
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA  
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT  
 CAGGAAATGACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA  
 GTGGAGCAAACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCCGGAGAAGAGACATCCT  
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG  
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC  
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTTGCAGCG  
 CCACGTTTCCCGCCACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA  
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC  
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA  
 GCGGCTCCAGGAGTTCCTTGCAGACATGGGTCTTCCCCTGAAGCAGGTGAAGCAGAAGTTCC  
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAATAAA  
 TTTGGGATGAAGGACATGCGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAAGCACAAAGTT  
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT  
 CAGGGACAGATCACTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG  
 TACCATGGCCTGGAACCTCGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC  
 CTTTGCACCAACCTCGTCATCTCCAGGGGCCTTTTCTGTACTGCTCTCTCATGGAGGGCAC  
 TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA  
 AGTCCTTTGTGTGTTTCGACAAAGAACCGGCGCTGCAAACCTGCTGCCCCCTGGTGATGGCTGCC  
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC  
 GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA  
 TGCTGCACAACCATTTTGGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT  
 CTGGACGCACTTATTTCCCTCCTGTCC**TAG**GAATTTGATTCTTCCAGAATGACCTTCTTATT  
 TATGTAACCTGGCTTTTCAATTTAGATTGTAAGTTATGGACATGATTTGAGATGTAGAAGCCATT  
 TTTTATTAAATAAAATGCTTATTTTAGGAAA

**FIGURE 27**

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF  
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD  
LEVPAIEDIFRDEEEDEEHSGNDS DGSEPSEKRTRLEEEIVEQTMRRRQRREWEARRRDILF  
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLQRH  
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLCNTSYTAARFKLWSVHGQKR  
LQEF LADMGLPLKQVKQKFQAMDISLKENLREMIIEESANKFGMKDMRVQTF SIHFGFKHKFL  
ASDVVFATMSLMESPEKDGS GTDHF IQALDSLRSNLDKLYHGLELAKKQLRATQQT IASCL  
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP  
LSMEHGT VTVVG IPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL  
DALISLLS

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**FIGURE 28**

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA  
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT  
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT  
GGTTCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTTCTTGAGCATAAAGAACAGTTTC  
ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT  
GAAGACACTATATTCTTTGTGTGTGACACCCATAGGCCAGTCAATGTTGTCAATGTATACAA  
CGATACCC

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**FIGURE 29**

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAAC  
 CACGAAGGGACGATACCAGAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG  
 GCTGACTTTTGGCTATAGAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGAAAGCTAA  
 GTCTTCCCTTTATCGAGTCAAGAAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAATT  
 GAGTAAAGTACGCTCCGGTCACC**ATG**GTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTC  
 CTGCTCTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGC  
 CAGCGGCTGCCAACGGTGCTGTGACTCTGAGGACCCCCCTGGATCCTGCCCATGTATCCTCAG  
 CCTCTTCCCTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTACATTAATATCACCATC  
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGG  
 TCCCCAAGGGGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCG  
 GCGCCCCGTGCCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGC  
 GGCAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA  
 CATGGCGACCCGGCCAGTTTGGTGTCTCCCTGCGTGGCATCTACTTCTTACGCCTCAATGTGC  
 ACAGTGGGAATTACAAGGAGCGTACGTGCACATTATGCATAACCAAGAGGGCTGTCTATC  
 CTGTACGCGCAGCCCAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGC  
 CTACGGGGACCGCGTCTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCA  
 ACGACTTCGACACCTACATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACT**GA**GGG  
 CCTCTGGGCCACCCTCCCGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG  
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATTTCTGGGGAGA  
 CCTGCTTCTATCTTGGCTGCCATCATCCCTCCAGCCTATTTCTGCTCCTCTCTTCTCTCT  
 TGGACCTATTTTAAAGAAGCTTGCTAACCTAAATATTCTAGAACTTTCCAGCCTCGTAGCCC  
 AGCACTTCTCAAACCTTGGAATGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCT  
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCCCTGGGTGATGCTG  
 ATGGGGTCAGTCTATGAACCACACTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAG  
 TACTTTCTGAACATTCTGGAATCCTCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTTCT  
 TGAGACAGAGTCTTGCTCTGTTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCAGTGC  
 AACCTCTGCCTCCCGGGTTCAAGCGATTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTAC  
 AGGCGCCTGCTACCATGCCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTACCATA  
 TTGGCCAGGCTGGTCTTGAACCTCCTGACTTCAGGTGACCCACCCGCCCTCGGCCCTCAA  
 GTGGGATTACAGGTGTGAGCCACCGTGCCTGGCCAATTCCAACATTCTTAAATTCTCTCAT  
 CCTCCAGGGCTCCCCGTGCTATGTTCTCTTTACCCCTTCCCCCTCTTCTCTTGCTCAGGCC  
 TGCACCACTGCAGCCACCGTTTCAATTTATTCATTCAATAAACAAGTACTCACTCTGTGCT  
 GGGTCCCCGGGAAGGGTGAGGGGGTGCAGACACAGGCCCTGCCCTGCCCTCAGTGAAGTGGCC  
 GTCCAGCCCAGGCGGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCCAGAGCTCATGGGG  
 GCCTGTGTTCTGGGTGTTTCAAGGTGCTGCTGGTCCCTCCATTACCCACTGCTCCCCAAGGCTGG  
 TGGGACGGGGTCCCGGTGGCAGGGGGCAGGTATCTCCTTCCCGTTCCTCATCCACCTGCCAG  
 TGCTCATCGTTACAGCAAACCCAGGGGGCCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG  
 ACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGCCCCGAAGAATGGAACCCACACCCA  
 TAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAGACCTGCCCTCCTCACTGGGATCCC  
 CTTCTGCTCCTCCCAGGGCTCTGCCAGGGCCTTGCTCAGTCCCTTCCACCAAAGTCACTCT  
 GAACTTCCGTTTCCCCAGGGCCTCCAGCTGCCCTCAGACACTGATGTCTGTCCCCAGGTGCT  
 CTCTGCCCTCATGCCCTCTCACCGGCCAGTGGCCCGACTCTCCAGGCTTTATCAAGGTG  
 CTAAGGCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCCTCCTCCGGCCTGGTGTGCTGCCCTTAC  
 AAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGAGCCCTCAGCAGGTCTGGGG  
 AGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCGTTTCTTCTTCCAGGGTGGGGTGGCCTGGT  
 GTTCCCCTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAGAGGGAGGCGGCCTCCGC  
 CCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCCGGGGGGTGATCTCTGGTGCTCAC  
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGGCAGGA  
 AGACCTGTGCTATAAACCACCCTGCCTGATCCTGCCCTGCCTGACCCCGCCACGCCCTGCC  
 GTCCAGCATGATTAAAGAATGCTGTCTCCTCTTGAAAAA

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[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]

**FIGURE 31**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCGACCCGCCAGGAAAGACTG  
 AGGCCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCCGCCCTCCCGGGACAGAAG**ATGTG**  
 CTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGGTGCAGG  
 GCTGCCCATCCGGCTGCCAGTGCCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG  
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT  
 CACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCTGCAGCTCCTGGACCTGTCAC  
 AGAACCAGATCGCCAGCCTGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTG  
 GACCTGACGGCCAACAGGCTGCATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCT  
 CGAGCGCCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCCTGGTGCCTTCGACACGC  
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCCGCTGCGC  
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCCGGCAT  
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG  
 AGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAG  
 CGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACAC  
 CCGCATTGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATG  
 TGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCTGCGG  
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGGCCCCCTG  
 GGTGCGCGAGAGCCACGTCACTTGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCCGCCCA  
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCACC  
 ACCACAGCCACAGTGCCCAACACGAGGCCCCGTGGTGCGGGAGCCACAGCCTTGTCTTCTAG  
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCA  
 CTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC  
 AATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTT  
 CACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTCA  
 CGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGC  
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA  
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG  
 AGTACACGGTCACCCAGCTGCGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGG  
 CCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTGCGGGGAGGCCATACACCCCCAGCCGTCCA  
 CTCCAACCACGCCCCAGTCACCCAGGCCCCGAGGGGCAACCTGCCGCTCCTCATTGCGCCCG  
 CCCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGG  
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCCT  
 GGAAGTGGAGGGAGTGAAGGTCCCCTTGGAGCCAGGCCCCGAAGGCAACAGAGGGCGGTGGAG  
 AGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTC  
 CAGTCACCCCTCCACGCAAAGCCCTACAT**CTAA**GCCAGAGAGAGACAGGGCAGCTGGGGCCG  
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCC  
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA  
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAAC  
 CGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG  
 GGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCCACTCCAGGCGGA  
 CCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTG  
 TGAAGTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTA  
 GGAACATGTTTTGCTTTTTTAAAATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG  
 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTTGTAAGACAAACGATGATATG  
 AAGGCCTTTTGTAAGAAAAAATAAAAGATGAAGTGTGAAA

**FIGURE 32**

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVFEN  
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR  
RLERLYLGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP  
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLVDSDNQLERVPPVIRGLRGLTRLRLAG  
NTRIAQLRPEDLAGLAALQELDVSNLSQLALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG  
PWVRESHVTLASPEETRCHFPPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS  
SSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHLACLCPE  
GFTGLYCESQMGQGTRPSPTPVTPRPPRSITLGIEPVSPTSRLRVGLQRYLQGSSVQLRSLRL  
TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPA  
VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQVGPGAG  
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI

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**FIGURE 33**

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT  
 CTTTCATCATTCATATGAGGAAATAAGTGGTAAAATCCTTGGAAATACA**ATG**AGACTCATCAG  
 AAACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAG  
 AAGAAAGGGAACTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTG  
 ACCCCAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTTCAACTCCAGAGTTCAGA  
 TTTTCATTCTGTCTCCAAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCAACAGCTGG  
 ATCTCAAAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTG  
 AAGAGTGTAACCTGGTATTTACTGGCAGGCTCAGGTATTTAGATCTTTCTTTAATGACTT  
 TGACACCATGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGA  
 GTGGGGGCAAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTC  
 TTCTTAGGATTCAGAACTCTTCCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAAC  
 AAAACTGCACATTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGGCGTGATGGAATCA  
 AGACTTCAAAAATATTAGAAATGACAAATATAGATTGGCAAAAGCCAATTTGTAAGTTATGAA  
 ATGCAACGAAATCTTAGTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA  
 TTTACTCTGGGACGACCTTTTCCTTATCTTACAATTTGTTTGGCATAACATCAGTGGAACT  
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTAC  
 TCAAACTACTGTAATGAGAACTATAAAATGGAGCATGTACATTTTCAAGAGTGTTTTACATTCA  
 ACAGGATAAAATCTATTTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAATG  
 CACAAATGCCACACATGCTTTTCCGAATTTATCTACGAAATTTCAATATTTAAATTTTGCC  
 AATAATATCTTAACAGACGAGTTGTTTAAAAGAACTATCCAACCTGCCTCACTTGAAAACCTCT  
 CATTTTGAATGGCAATAAACTGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACAC  
 CCTTGGAACACTTGGATCTGAGTCAAAATCTATTACAACATAAAAATGATGAAAATTGCTCA  
 TGGCCAGAACTGTGGTCAATATGAATCTGTACATAATAAATTGTCTGATTTCTGTCTCAG  
 GTGCTTGGCCCAAAAGTATTTCAAATACTTGACCTAAATAATAACCAATCCAACTGTACCTA  
 AAGAGACTATTCATCTGATGGCCTTACGAGAACTAAATATTGCATTTAATTTTCTAACTGAT  
 CTCCTTGGATGCAGTCATTTTCACTAGACTTTTCACTTCTGAACATTGAAATGAACCTTCATTCT  
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACTCTAAATGCCGGGAAGAA  
 ATCCATTTCCGGTGTACCTGTGAATTAATAAATTTTCACTCAGCTTGAAACATATTCAGAGGTC  
 ATGATGGTTGGATGGTCAGATTCATACACCTGTGAATACCTTTTAAACCTAAGGGGAAGTAG  
 GTTAAAAGACGTTTCTCTCCACGAATTATCTTGCAACACAGCTCTGTTGATTGTCACCATTG  
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCTTCTGCTGTCTCCACTTTGATCTGCCC  
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAACAACCCA  
 AGAACAACTCAAGAGAAATGTCCGATTTCCACGCATTTATTTTATACAGTTGAACATGATTTCT  
 TGTGGGTGAAGAATGAATTGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTTGC  
 CTTTATGAAAGCTACTTTGACCCTGGCAAAAGCATTAGTGAAAATATTGTAAGCTTCATTGA  
 GAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCAACTTTGTCCAGAATGAGTGGTGCCATT  
 ATGAATTTACTTTGCCCACCACAATCTCTTCCATGAAAATTTCTGATCATATAATCTTATC  
 TTAATGGAACCCATTCCATTCTATTGCAATTTCCACCAGGTATCATAAACTGAAAGCTCTCCT  
 GGAAAAAAAGCATACTTGGAATGGCCCAAGGATAGGCGTAAATGTGGGCTTTTCTGGGCAA  
 ACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCAGAGAAATGTATGAACTGCAGACA  
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTGTCT  
**ATA**AAATCCCACAGTCCTTGGGAAGTTGGGGACCACATACTGTTGGGATGTACATTGATA  
 CAACCTTTATGATGGCAATTTGACAATATTTATTAATAAATAAATAAATGGTTATTTCCCTTCATA  
 TCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACACCTTCACAAGTTTATAAGG  
 GCTTATGAAAAAGGTGTTTCTCCAGGATTGTTTATAATCATGAAAAATGTGGCCAGGTGC  
 AGTGGCTCACTCTTGTAATCCCAGCACTATGGGAGGCCAAGGTGGGTGACCCACGAGGTCAA  
 GAGATGGAGACCATCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAATTA  
 GCTGGGCGTGATGGTGACGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATCG  
 CTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTGCACTCCAGCCTGGT  
 GACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAATGGAAAACATCC  
 TCATGGCCACAAAATAAGGTCTAATTCAATAAATTATAGTACATTAATGTAATATAATATTA  
 CATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTTGGTATGGAAAAACATATTAATAT  
 GTTATAAACTATTAGGTTGGTGCAAACTAATTGTGGTTTGGGTTTGGCATTGAAATGGCATTGAA  
 ATAAAAGTGTAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGTCTGGGAGGTTGGA  
 TTACAGGGAGCATTTGATTTCTATGTTGTGATTTCTATAATGTTTGAATTGTTTAGAATGA  
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

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**FIGURE 34**

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ  
LQSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL  
SFNDFDTPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP  
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL  
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR  
VFYIQQDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNfANNILTDELfKRTIQLP  
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNdENCsWPETVVNMNLSYNKLS  
DSVFRCLPKSIQILDlNNNqIQTVPKETIHLMAlRELNIaFNfLTDLPgCSHFsrLSVLNIE  
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN  
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFcCLHFDLPWYLRMLGQCTQTWHRV  
RKTTQEQlKRNVRfHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI  
VSFIEKSYKSIFVLSPNFVQNEWCHYEFYFAHhNLFHENSdHIILILLEPIPFYCIPTRYHK  
LKALLEKKAYLEWPKDRRKGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM  
RTDCL

**FIGURE 35**

GGGGGCTTTCTTGGGCTTGGCTGCTTGGAAACACCTGCCTCCAAGGACCGGCCTCGGAGGGGTGCGCCGGGAAAGG  
 GAGGGAAGAAGGAAGGGCGGGGCCGCCCCCTGCGCCCGCCCGCGCCTCTGCGCGCCCCCTGTCCGCCCCGGC  
 CCAGCCCAGCCCAGCCCCGCGGGCCGGTACACGCGCAGCCAGCCGCGCCCTCCCGCGCCCAAGCGCGCCGCT  
 CTGCTGTGCCCTGCGCCCTTGCCCCGCGCCAGCTTCTGCGCCCGCAGCCCGCCCGCGCCCCGGTGACCGTGA  
 CCCTGCCCTGGGCGCGGGGCGGAGCAGGC**ATG**TCCCGCCCGGGGACCGCTACCCAGCGCTGGCCCTGGTGCTC  
 CTGGCAGTGACCTGGCCGGGGTGGAGCCAGGGCGCAGCCCTCGAGGACCTGATTATTACGGGCAGGAGAT  
 CTGGAGCCGGGAGCCCTACTACGCGCGCCCGAGCCGAGCTCGAGACCTTCTCTCCGCGCTGCTGCGGGGC  
 CCGGGGAGGAGTGGGAGCGCGCCCGCAGGAGCCAGGCCGCCAAGAGGGCCACCAAGCCCAAGAAAGCTCCC  
 AAGAGGGAGAAGTCGGCTCCGGAGCCGCTCCACCAGGTAACACAGCAACAAAAAGTTATGAGAACCAAGAG  
 CTCTGAGAAGGCTGCCAACGATGATCACAGTGTCGTGTGGCCCGTGAAGATGTCAGAGAGAGTTGCCACCTC  
 TTGGTCTGGAAACCTTAAAAATCACAGACTTCCAGCTCCATGCCTCCACGGTGAAGCGCTATGGCCTGGGGGCA  
 CATCGAGGGAGACTCAACATCCAGGCGGGCATTAATGAAATGATTTTATGACGGAGCGTGGTGCGCGGGAAG  
 AAATGACCTCCAGCAGTGGATTGAAGTGGATGCTCGGCGCCTGACCAGATTCACTGGTGTCACTCAAGGGA  
 GGAACCTCCCTCTGGCTGAGTGACTGGGTGACATCCTATAAGGTGATGGTGAGCAATGACAGCCACAGTGGGTG  
 ACTGTTAAGAATGGATCTGGAGACATGATATTTGAGGGAAACAGTGAGAAGGAGATCCCTGTTCTCAATGAGCT  
 ACCCGTCCCCATGGTGGCCCGTACATCCGCATAAAACCTCAGTCCTGGTTTGATAATGGGAGCATCTGCATGA  
 GAATGGAGATCCTGGGCTGCCCCACTGCCAGATCCTAATAATTATTATCACCGCCGGAACGAGATGACCACCACT  
 GATGACCTGGATTTTAAGCACCACAATTATAAGGAAATGCGCCAGTTGATGAAAGTTGTGAATGAAATGTGTCC  
 CAATATCACCAAGATTTTACAACATTGGAAGAAAGCCAGGGCCTGAAGCTGTATGCTGTGGAGATCTCAGATC  
 ACCCTGGGGAGCATGAAGTCGGTGAGCCCGAGTTCCACTACATCGCGGGGGCCACGGCAATGAGGTGCTGGGC  
 CGGGAGCTGCTGCTGCTGCTGGTGACGTTTCGTGTGTGAGGAGTACTTGGCCCGGAATGCGCGCATCGTCCACCT  
 GGTGGAGGAGACGCGGATTACGTCCTCCCTCCCTCAACCCCGATGGCTACGAGAAGGCCCTACGAAGGGGGCT  
 CGGAGCTGGGAGGCTGGTCCCTGGGACGCTGGACCCACGATGGAATTGACATCAACAACAACCTTTCCTGATTTA  
 AACACGCTGCTCTGGGAGGCGAGGATCGACAGAATGTCCCCAGGAAAGTTCCCAATCACTATATTGCAATCCC  
 TGAGTGGTTTCTGTGCGGAAATGCCACGGTGGCTGCCGAGACCAGAGCAGTCATAGCCTGGATGGAAAAATCC  
 CTTTTGTGCTGGGCGGCAACCTGCAGGGCGGCGAGCTGGTGGTGGCGTATCCCTACGACCTGGTGCGGTCCCC  
 TGGAAGACGCAGGAACACACCCCCACCCCCGATGACCAGCTGTTCCGCTGGCTGGCCTACTCCTATGCCTCCAC  
 ACACCGCCTCATGACAGACGCCCCGAGGAGGGTGTGCCACACGAGGACTTCCAGAAGGAGGAGGGCACTGTCA  
 ATGGGGCCTCCTGGCACACCGTCTGCTGGAAGTCTGAACGATTTTCACTACCTTCATACAACTGCTTCGAACTG  
 TCCATCTACGTGGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCCGAGGAGTGGGAGAATAACCGGGAATC  
 TCTGATCGTGTTTCATGGAGCAGGTTTCATCGTGGCATTAAAGGCTTGGTGAGAGATTACATGGAAAAGGAATCC  
 CAAACGCCATTATCTCCGTAGAAGGCATTAACCATGACATCCGAACAGCCAACGATGGGGATTACTGGCGCTC  
 CTGAACCTTGAGAGTATGTGGTACAGCAAAGGCCGAAGGTTTCACTGCATCCACCAAGAAGTGTATGGTTGG  
 CTATGACATGGGGGCCACAAGGTGTGACTTCACTTAGCAAACCAACATGGCCAGGATCCGAGAGATCATGG  
 AGAAGTTTGGGAAGCAGCCCGTCAAGCTGCCAGCCAGGCGGCTGAAGCTGCGGGGGCGGAAGAGACGACAGCGT  
 GGG**TGA**CCCTCCTGGGCCCTTGAGACTCGTCTGGGACCCATGCAAATTAAACCAACCTGGTAGTAGCTCCATAG  
 TGGACTCACTCACTGTTGTTTCTCTGTAATTCAAGAAGTGCCTGGAAGAGAGGGTGCATTGTGAGGCAGGTCC  
 CAAAAGGGAAGGCTGGAGGCTGAGGCTGTTTTCTTTCTTTGTTCCCATTTATCCAAATAACTTGGACAGAGCA  
 GCAGAGAAAAGCTGATGGGAGTGAGAGAACTCAGCAAGCCAACTGGGAATCAGAGAGAGAAGGAGAAGGAGGG  
 GAGCCTGTCCGTTTCAAGCCTCTGGCTGCATAGAAAAGGATTCTGGTGCTTCCCCTGTTTGGCTGGCAGCAAGG  
 GTTCCACGTGCATTTGCAATTTGCACAGCTAAAATTGCAGCATTTTCCCAGCTGGGCTGTCCCAAATGTTACCA  
 TTTGAGATGCTCCAGGCGTCCTAAGAGAATCCACCTCTCTGGCCCTGGGACATTGCAAGCTGCTACAAATAA  
 ATTCTGTGTTCTTTTGACAATAGCGTCATTGCCAAGTGCACATCAGTGAGCCTCTTGAATCTGTTTAGTCTCCT  
 TTTTCAACAAAGGAGTGTGTTTCAAAAAGGAGAGAGAGGCTGAGATCATTAGGAGTTTGTGGGCAGCAAGCA  
 TGGAGCTTCTTGACAAATTCTGGGTCCATAAACAACCCCAAAGTCCCTGCTGATCCAGTAGCCCTGGAGGTT  
 CCCAGGTAGGGAGAGCCAGAGGTGCCAGCCTTCTGAAGGGCCAGAAAATTTAGCCTGGATCTCCTCTTTTAC  
 CTGCTAGGACTGGAAAGAGCCAGAAGTGGGGTGGCCTGAAGCCCTCTCTGCTTGGGTATTGCCCTGTGTG  
 GAATTGAGTGCTCATGGGTTGGCCTCATATCAGCCTGGGAGTTATTTTGTATATGTAGAATGCCAGATCTTCCA  
 GATTAGGCTAAATGTAATGAAAACCTCTTAGGATTATCTGTGGAGCATCAGTTTGGGAAGAATTATTGAATTAT  
 CTTGCAAGAAAAAAGTATGTCTCACTTTTTGTAAATGTTGCTGCCTATTGACCTGGGAAAAATGAAAAAAA  
 AATAAAGCAAATGGTAAGACCTTAAAAA

**FIGURE 36**

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPPLP  
AGPGEEWERRPQEPRPPKRA TKPKKAPKREKSAPEPPPPGKHSNKKVMRTKSSEKAANDDHS  
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRLNIQAGINENDFYDGAWCA  
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSTWVTVKNGSGDMIF  
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDPNNYYHRRNEMTT  
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF  
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG  
SELGGWSLGRWTHD GIDINNNFPDLNTLLWEAEDRQNVPRKVPNH YIAIPEWFLSENATVAA  
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYS YAST  
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFS YLHTNCFELSIYVGCDKYPHES  
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGIPNAIISVEGINHDIRTANDGDYWRLL  
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR  
LKLGRGRKRRQRG

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**FIGURE 37**

CTAAGAGGACAAGATGAGGCCCCGGCCTCTCATTTCTCCTAGCCCTTCTGTTCTTCCTTGGCCAAGCTGCAGGGG  
 ATTTGGGGGATGTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTTCCCAGGTGTTGACTCCAGCTCCAGC  
 TTCAGCTCCAGCTCCAGGTCCGGGCTCCAGCTCCAGCCGACGCTTAGGCAGCGGAGGTTCTGTGTCCCAGTTGTT  
 TTCCAATTTACCCGGCTCCGTGGATGACCGTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACCACCTTTC  
 CCGTGGACAGAGTGGAACGCTTGGAAATTCACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAGAACTTTCTAAA  
 GTGAGGGAATATGTCCAATTAATTAGTGTGTATGAAAAGAACTGTTAAACCTAACTGTCCGAATTGACATCAT  
 GGAGAAGGATACCATTTCTTACACTGAACCTGGACTTCGAGCTGATCAAGGTAGAAGTGAAGGAGATGGAAAAAC  
 TGGTCATACAGCTGAAGGAGAGTTTTGGTGGAGCTCAGAAATTGTTGACCAGCTGGAGGTGGAGATAAGAAAT  
 ATGACTCTCTTGGTAGAGAAGCTTGAGACACTAGACAAAAACAATGTCCTTGCCATTGCGCCGAGAAATCGTGGC  
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAAACACCCCTGTCGTCCACCCTCCTCCCACTC  
 CAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGTGGTTCAGCTCAACTGGAGAGGGTTT  
 TCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCCAGCATCCAAACAAAGGACTGTATTGGGTGGCGCC  
 ATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTACAACACACTGGATGATTTGCTATTGTATATAA  
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC  
 ATGTACAACACCGGGAATATTGCCAGAGTTAACCTGACCACCAACACGATTGCTGTGACTCAAACCTCCTCCTAA  
 TGCTGCCATATAATAACCGCTTTTCATATGCTAATGTGCTTGGCAAGATATTGACTTTGCTTGGATGAGAATG  
 GATTGTGGGTTATTTTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACCACACTT  
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCTTCATGGTATGTGGGGTTCT  
 GTATGCCACCCGTACTATGAACACCAGAACAGAAGAGATTTTTTACTATTATGACACAAACACAGGGAAGAGG  
 GCAAACCTAGACATTGTAATGCATAAGATGCAGGAAAAAGTGCAGAGCATTAACCTATAACCCTTTTGACCAGAAA  
 CTTTATGTCTATAACGATGGTTACCTTCTGAATTATGATCTTTCTGCTTGCAGAAGCCCCAGTAAAGCTGTTTA  
 GGAGTTAGGGTGAAAGAGAAAAATGTTTGTTGAAAAAATAGTCTTCTCCACTTACTTAGATATCTGCAGGGGTGT  
 CTAAAAGTGTGTTTCATTTTGCAGCAATGTTTAGGTGCATAGTTCTACCACACTAGAGATCTAGGACATTTGTCT  
 TGATTTGGTGAGTTCTCTTGGGAATCATCTGCCTCTTCAGGCGCATTTTGAATAAAGTCTGTCTAGGGTGGGA  
 TTGTCAGAGGTCTAGGGGCACTGTGGGCCTAGTGAAGCCTACTGTGAGGAGGCTTCACCTAGAAGCCTTAAATTA  
 GGAATTAAGGAACCTTAAACTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAAATATTGCCCAATGACTAGTC  
 CTCATCCATGTAGCACCCTAATTCTTCCATGCCTGGAAGAAACCTGGGGACTTAGTTAGGTAGATTAATATCT  
 GGAGCTCCTCGAGGGACCAAACTCTCCAACCTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG  
 CAGATAAGTAAATTTGGCATGCTTATATATTCTACATCTGTAAAGTGTGAGTTTTATGGAGAGAGGCCCTTTTT  
 ATGCATTAAATTGTACATGGCAAATAAATCCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTTCTTTCTCTC  
 ATTTGTCCACCTTACTAAAAGTCAGTAGAATCTTCTACCTCATAACTTCCTTCCAAAGGCAGCTCAGAAGATTAG  
 AACCAGACTTACTAACCAATTCCACCCCCACCAACCCCTTCTACTGCCTACTTTAAAAAATTAATAGTTTT  
 CTATGGAAGTATCTAAGATTAGAAAAATTAATTTCTTTAATTTTATTATGGACTTTTATTTTACATGACTCTA  
 AGACTATAAGAAAAATCTGATGGCAGTGACAAAGTGCTAGCATTATTGTTATCTAATAAAGACCTTGGAGCATA  
 TGTGCAACTTATGAGTGTATCAGTTGTTGCATGTAATTTTTGCCTTTGTTTAAGCCTGGAACCTTGAAGAAAAT  
 GAAAATTTAATTTTTTTTTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGT  
 TGGAAACCTTGCTGGTGTATGTGATGTGCTTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT  
 TCCTTTGATGTTCAAGTCCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCCCCCTTTTAAATAAATGAT  
 TAAATGTGCTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 38**

MRPGLSFL LALLFFLGQAAGDLGDVGPPIPSPGFS SPGVDSSSSSFSSSSSRSGSSSSRSLGS  
GGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV  
QLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ  
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPPPTPGSCGH  
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPQH PNKGLYWVAPLNTDGRLL EYYRLYNTLD  
DLLLYINARELRITYGQSGTAVYNNNMYVNM YNTGNIARVNLTNTIAVTQTLPNAA YNNR  
FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNTWYTKQYKPSASNAF  
MVCGLYATR TMNTRTEEIFYYYDTNTGKEGKL DIVMHKMQEKVQSINYNPFDQKLYVYNDG  
YLLNYDLSVLQKPQ

**FIGURE 39**

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC  
CCTCCTCCCCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT  
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC  
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG  
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT  
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA  
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

**FIGURE 40**

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTAT  
 CCGCTGCTCTTGTGACGTTGTGGAG**ATG**GGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCT  
 GGATACCATGTTTGTGTGGAAGTGCCCCGTGTTTGCTATGCCGATGCTGTCTAGTGGAAC  
 AACTCCACTGTAAC TAGATTGATCTATGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTG  
 TGTAATGTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCCTGGATTTTGTGAGAATG  
 AGAAAGGTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT  
 GGTTTGGCTATGTTCTATCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA  
 TCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTA  
 TTATTGGGGCATTCTTCATTCCAGAAGGAACCTTTTACAACCTGTGTGGTTTTATGTAGGCATG  
 GCAGGTGCCTTTTGTTCATCCTCATACAACCTAGTCTTACTTATTGATTTTGCACATTCATG  
 GAATGAATCGTGGGTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCAGCCTTGT  
 TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCCTGTTCTTTGTCTAC  
 TACACTCATCCAGCCAGTTGTTTCAAGAAACAGGCGTTTATCAGTGTCAACATAGTCTCCTCTG  
 TCTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTT  
 TGTTACAGTCTTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT  
 GAACCAGAAACAAATTGCAACCCAAGTCTACTAAGCATAATTGGCTACAATACAACAAGCAC  
 TGTCCCAAAGGAAGGGCAGTCAAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTAATTC  
 TCTTTTTGTGTGTGTATTTTATCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAA  
 CTGACTCTAACAAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATC  
 ACTGGAGGATGGGGACGATGTTTACCAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA  
 GTTATTCCTTCTTTCACCTTCATGCTTTTCTGGCTTCACCTTATATCATGATGACCCCTTACC  
 AACTGGTCCAGGTATGAACCCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA  
 AATCTCTTCCAGTTGGATTGGCATCGTGTATGTTTGGACACTCGTGGCACCCTTGTTC  
 TTACAATCGTGATTTT**GACTGAGT**GAGACTTCTAGCATGAAAGTCCCACTTGTATTATTGC  
 TTATTTGAAAACAGTATTCCCAACTTTTGTAAAGTTGTGTATGTTTTTGTCTCCCATGTAAC  
 TTCTCCAGTGTTCTGGCATGAATTAGATTTTACTGCTTGTCAATTTTGTATTCTTACC  
 GTGCATTGATATGTGAAGTAGAATGAATTGCAGAGGAAAGTTTTATGAATATGGTGATGAGT  
 TAGTAAAAGTGGCCATTATTGGGCTTATTCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA  
 ACAATTTTGTGTTGACTATTTTAAATTAATTTAGACCTTAAGCTGTTTGTAGCAAGCATTAAA  
 GCAAATGTATGGCTGCCTTTTGAATATTTGATGTGTTGCCTGGCAGGATACTGCAAAGAAC  
 ATGGTTTATTTTAAATTTTATAAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA  
 AGGTTTTTACCCTTGATACGGAATTTACACAGGTAGGGAGTGTTTAGTGGACAATAGTGTAGG  
 TTATGGATGGAGGTGTCGGTACTAAATTGAATAACGAGTAAATAATCTTACTTGGGTAGAGA  
 TGGCCTTTGCCAACAAAGTGAACGTGTTTTGGTTGTTTTAAACTCATGAAGTATGGGTTCACT  
 GGAAATGTTTGGAACCTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGA  
 AGGAAGTGTGTTTGAAGTCACTTTGAAAGTTAGTTTTGGGCCAGCACGGTAGCTCACCCCTT  
 GGTAATCCCAGCACTTTGGGAGCTTAAGTGGGTAGATTACTTGAGCCCAGGAATTCAGACCA  
 GCTTGGCACATGGTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCCTGTGGTC  
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCAGAGCCAAAGGTTGCAGTGAGCAAGTCA  
 CGTCACTGCACTCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATATTGAAATCAAGG  
 AGGCAAAATTTTGAAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTAT  
 ATAAAATCTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA  
 GCTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATAATAGCATTCTCTCTGACATTTAA  
 AAATAATTTCTATTCAAATAACATGCATATTGATTTACACCTCATACTGTGATAATTAATGT  
 GATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAAGAATGATGGAATGTTTT  
 AGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAAGATGTTTAAATGCTTTTGTAT  
 TTAGTGGCATGTAATTGAAATATATAGATTATTGTAACCTTTCAACCTGAAAATCAAGCAGT  
 ATGAGAGTTTAGTTATTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTACAATT  
 TCTTCTTTAAAAATATTTATTAATGTGAATGGAATATAACAATTCAGCTTAATTCCCCAACCC  
 TTATTCTGTGTGTAGACATTGTATTCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAA  
 ATGAATTCAGAGAAAAA

**FIGURE 41**

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME  
EQLNKIPGFCENEKGVVPCNILVGKYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNG  
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKM  
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLCVGASVMSI  
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV  
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH  
RAVDNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVWVKISSSWIGI  
VLYVWTLVAPLVLNDRFD

**FIGURE 42**

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT  
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC  
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGGAACAANTCCACTGTAACTAGATTGATCTA  
TGCACTTTTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG  
AACAACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT  
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT  
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT  
TTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC

**FIGURE 43**

GTTATTGTGAAC TTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC  
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAAACAANTCC  
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTTGGAGTANGTGTAGCTTGTGTAAT  
GTTGATACCAGGAATGGAAGAACA ACTGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG  
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG  
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG  
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTTGCTGCAGCAATTGCAATTATTATTG  
GGGC

**FIGURE 44**

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC  
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGTT  
TGCTATGCCGATGCTGTCCTAGTGGAAACAACCTCCACTGTAAGTAGATTGATCTATGCACTT  
TTCTTGCTTGTGAGATATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACCT  
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATTTTGGTTG  
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTCTTTA  
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT  
CTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGC



**FIGURE 45**

GCTGTCCTTAGTGGAAACAANTCCAACCTTGTAACCTGGATTGATCTATGCACTTTTTTCCTTG  
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCAGGATTGGANGAACAACTGAATA  
AGATTCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCCTTGTAACATTTTTGGTTGGC  
TATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCTCTTTACT  
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT  
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTTT  
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACCTAGT  
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAAATGGAAGAAGGGA  
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA  
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC  
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

**FIGURE 46**

CTCGGGCGCGCACAGGCAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCTCGGGCCGCGCCGCTCTCCAAT  
GGCAAATGTGTGTGGCTGGAGGCGAGCGCGAGGCTTTTCGGCAAAGGCAGTCGAGTGTTCAGAGACCGGGGCGAG  
TCCTGTGAAAGCAGATAAAAGAAAACATTTATTAACTGTCTATTACGAGGGGAGCGCCCGGGGCTGTGCG  
ACTCCCCGCGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAAGAAGAAAGCGGAAAAGAGGCAGATTAC  
GTCGTTTCCAGCCAAGTGGACCTGATCGATGGCCCTCCTGAATTTATCAGATATTTGATTTATTAGCGATGCC  
CCCTGCTTTGTGTGTACGCACACACACGTGCACACAAGGCTCTGGCTCGCTTCCCTCCCTCGTTTCCAGCTCC  
TGGGCGAATCCACATCTGTTTCAACTCTCCGCCGAGGGCGAGCAGGAGCGAGAGTGTGTGCAATCTGCGAGTG  
AAGAGGGACGAGGGGAAAAGAAACAAAGCCACAGACGCAACTTGAGACTCCCGCATCCCCAAAAGAACACAGAT  
CAGCAAAAAAAGAAAGATGGGGCCCCCGAGCCTCGTGCTGTGCTTGTGTGCTGTCGCAACTGTGTTCTCCCTGCTGGG  
TGGAAGCTCGGCCTTCTGTGCGCACCACCGCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCCA  
ACATCATCTCTGGTGTGACGGACGACCAGGATGTGGAGCTGGGTTCCATGCGAGGTGATGAACAAGACCCGGCGC  
ATCATGGAGCAGGGCGGGGCGCATTTCATCAACGCCCTCGTGACCACACCCATGTGCTGCCCTCACGCTCCTC  
CATCCTCACTGGCAAGTACGTCCACAACCACAACACCTACACCAACAATGAGAACTGCTCCTCGCCCTCCTGGC  
AGGCACAGCAGGAGCGGCACCTTTGCCGTGTACCTCAATAGCACTGGCTACCGGACAGCTTTCTTCGGGAAG  
TATCTTAATGAATACAACGGTCTCTACGTGCCACCCGCTGGAAGGAGTGGGTGCGACTCCTTAAAAACTCCCCG  
CTTTTATAACTACACGCTGTGTCGGAACGGGGTGAAGAGAAGCACGGCTCCGACTACTCCAAGGATTACCTCA  
CAGACCTCATACCAATGACAGCGTGAGCTTCTTCCGCACGTCCAAGAAGATGTACCCGCACAGGCCAGTCCCTC  
ATGGTCATCAGCCATGCAGCCCCCAGGGCCCTGAGGATTACGCCCCACAATATTACGCTCTTCCCAAACGC  
ATCTCAGCACATCAGCCGAGCTACAACACGCGCCCAACCCGGACAAACACTGGATCATGCGCTACACGGGGC  
CCATGAAGCCCATCCACATGGAATTCACCAACATGCTCCAGCGGAAGCGCTTGCAGACCTCATGTGCGTGGAC  
GACTCCATGGAGACGATTACAAACATGTGTTGAGACGGGCGAGCTGGACAACACGTACATCGTATACACCGC  
CGACCACGGTTACACATCGGCCAGTTTGGCCTGGTGAAGGGGAAATCCATGCCATATGAGTTTGACATCAGGG  
TCCCGTTCTACGTGAGGGGCCCCAACGTGGAAGCCGGCTGTCTGAATCCCCACATCGTCTCAACATTGACCTG  
GCCCCACCATCCTGGACATTGCAGGCCTGGACATACCTGCGGATATGGACGGGAAATCCATCCTCAAGCTGCT  
GGACACGGAGCGGCGGCTGAATCGGTTTCACTTGAAAAAGAGATGAGGGTCTGGCGGGACTCCTTCTGGTGG  
AGAGAGGCAAGCTGTACACAAGAGAGACAATGACAAGGTGGACGCCCAGGAGGAGAACTTTCTGCCAAGTAC  
CAGCGTGTGAAGGACCTGTGTACGCGTGTGAGTACCAGACGGCGTGTGAGCAGCTGGGACAGAAGTGGCAGTG  
TGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGCAAGGGCCCCATGCGGCTGGGCGGCAGCAGAGCCC  
TCTCCAACCTCGTGCCCAAGTACTACGGGCAGGGCAGCGAGGCCTGCACCTGTGACAGCGGGGACTACAAGCTC  
AGCCTGGCCGGACGCCGAAAAAACTCTTCAAGAAGAAGTACAAGGCCAGCTATGTCCGCGAGTCGCTCCATCCG  
CTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCACGTAGGCCTGGGTGATGCCGCCAGCCCCGAAACCTCA  
CCAAGCGGCACTGGCCAGGGGCCCCCTGAGGACCAAGATGACAAGGATGGTGGGGACTTCAGTGGCACTGGAGGC  
CTTCCCGACTACTCAGCCGCCAACCCATTAAAGTGACACATCGGTGCTACATCCTAGAGAACGACACAGTCCA  
GTGTGACCTGGACCTGTACAAGTCCCTGCAGGCCTGGAAGACCACAAGCTGCACATCGACCACGAGATTGAAA  
CCCTGCAGAACAAAATTAAGAACCTGAGGGAAGTCCGAGGTACCTGAAGAAAAAGCGGCCAGAAGAATGTGAC  
TGTCACAAAATCAGCTACCACACCCAGCACAAAGGCCGCTCAAGCACAGAGGCTCCAGTCTGCATCCTTTTCAG  
GAAGGGCCTGCAAGAGAAGGACAAGGTGTGGCTGTTGCGGGAGCAGAAGCGCAAGAAGAACTCCGCAAGCTGC  
TCAAGCGCCTGCAGAACACGACACGTGCAGCATGCCAGGCCTCACGTGCTTCACCCACGACAACCGCACTGG  
CAGACGGCGCCTTTCTGGACACTGGGGCCTTTCTGTGCTGCACCAGCGCCAACAATAACACGTACTTGTGAT  
GAGGACCATCAATGAGACTCACAATTTCTCTTCTGTGAATTTGCAACTGGCTTCTAGAGTACTTTGATCTCA  
ACACAGACCCCTACCAGCTGATGAATGCAGTGAACACACTGGACAGGGATGTCTCAACCAGCTACACGTACAG  
CTCATGGAGCTGAGGAGCTGCAAGGGTTACAAGCAGTGTAACCCCCGACTCGAAACATGGACCTGGATGGAGG  
AAGCTATGAGCAATACAGGCAGTTTCAGCGTCGAAAGTGGCCAGAAATGAAGAGACCTTCTTCAAATCACTGG  
GACAACTGTGGGAAGGCTGGGAAGGTTAAGAAACAACAGAGGTGGACCTCCAAAAACATAGAGGCATCACCTGA  
CTGCAAGGCAATGAAAAACCATGTGGGTGATTTCCAGCAGACCTGTGCTATTGGCCAGGAGGCCTGAGAAAGC  
AAGCACGCACTCTCAGTCAACATGACAGATTCTGGAGGATAACCAGCAGGAGCAGAGATAACTTCAGGAAGTCC  
ATTTTTGCCCTGCTTTTGTGTTTGGATTATACCTCACCAGCTGCACAAAATGCATTTTTTCGTATCAAAAAGTC  
ACCACTAACCTCCCCAGAAGCTCACAAGGAAAACGGAGAGAGCGAGCGAGAGAGATTTCTTGGAAATTTCT  
TCCAAGGGCGAAAGTCATTGGAATTTTAAATCATAGGGGAAAAGCAGTCCTGTTCTAAATCCTCTTATTCTT  
TTGGTTTGTCAAGAAAGGAACATAAGAAGCAGGACAGGGAACGTGGAGAGGCTGAAAACAGTGCAGAGACG  
TTTGACAAATGAGTCAGTAGCACAAAAGAGATGACATTAGCTAGCACTATAAACCTGGTTGCCTCTGAAGAAA  
CTGCCTTCATTGTATATATGTGACTATTTACATGTAATCAACATGGGAACCTTTTAGGGGAACCTAATAAGAAAT  
CCCAATTTTCAGGAGTGGTGGTGTCAATAAACGCTCTGTGGCCAGTGTAAGAAAAA

**FIGURE 47**

MGPPSLVLCLLSATVFSLGGSSAFLSHHRLKGRFQRDRRNIRPNIILVLTDDQDVELGSMQ  
VMNKTRRIMEQGGAHFINAFVTTPMCCPSRSSILTGKYVHNHNTYTNNECSPSWQAQHE  
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD  
YSKDYLTDLITNDSVSFFRTSKKMPHRPVL MVISHAAPHGPEDSAPQYSRLFPNASQHITP  
SYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQKRKLQTLMSVDDSMETIYNMLVETGELDNT  
YIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPVNEAGCLNPHIVLNIDLAPTILDI  
AGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN  
FLPKYQVRVLDLCQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKY  
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSV AIEVDGRVYHVGLGDAAQ  
PRNLTKRHWP GAPPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS  
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRLKHRGSSL  
HPFRKGLQEKDKVWLLREQKRKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG  
PFCACTSANNNTYWCMRTINETHNFLCFEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL  
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

**FIGURE 48**

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA  
GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCCAG**ATG**CTGGGCCTCCTGGGGAGCACAGCCC  
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCCTGCTGCTGCTGCTGCTGCTGGCCACC  
TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA  
CCGAGTCCGCCGGGCCCCAGCCTTGGCCCTTCCGGCGGGGGGCCACCTGGGAATCTTTCACC  
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC  
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCA  
CGCTCGC**TGA**GGCTGCTGTGCCGGTGCCTGTGGACAGCAGCTGCCCCCTGCCCTCCCATCTG  
TCCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG  
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTACTATGGC  
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG  
GTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGAAGTCCCAGTGAGCCCCAGAAATG  
ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC  
ATCAGGCTGCTGCAGGCCTCTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT  
GGTTTGGAGAAGGCAGTGTGAGGCTGCACAGTCAATTATCGGTGCCTTAGTCCAAGAAAAT  
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

**FIGURE 49**

MLGLLGSTALVGWITGAAVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRAPWPFR  
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPRHHHPRHAR

Protein Data Bank

**FIGURE 50**

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTA  
CTACTGGGCCTGATTGGGGGCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG  
GTACTCAGGGCTACTGGCTGGGGTGGAAGTGAGTGCTGGGTCACCCCCCATCCGCAACGTCA  
CTGTGGCCTACAAGTTCCACATGGGGCTCTATGGTGAGACTGGGCGGCTTTTCACTGAGAGC  
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC  
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC  
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC  
CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG  
TGTCCATCCTGCCTTGGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG  
AGATCTACCAGGAAGACCAGATCCATTTTATGTGCCCACTGGCACGGCAGGGAGACTTCTAT  
GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA  
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAGTGAGCC  
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGGGGCGAGCAGCCGTGGCTGGGAT  
GACGGTGACACCCGCAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA  
GGAGCTGGACTTGGAGGGCGAGGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC  
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCCCTGAGAAGGGCAAGGAGTAACCC  
ATGGCCTGCACCCTCCTGCAGTGCAGTTGCTGAGGAACTGAGCAGACTCTCCAGCAGACTCT  
CCAGCCCTCTTCCTCCTTCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC  
TCCAGGCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA  
GGGACTATTTTCTGCACCAGCCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTTTCAGACTC  
ACAGTGGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTTCACCTGGAAAAAA  
AAAAA

**FIGURE 51**

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR  
LFTESCSISPKLRSIAVYYDNPHMVPPDKCRCAVGSILSEGEESPSPELIDLYQKFGFKVFS  
FPAPSHVVTATFPYTTILSIWLATTRVHPALDTYIKERKLCAYPRLIYQEDQIHFMCPAR  
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSATLSPGAS  
SRGWDDGDTRSEHSYSESGASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK  
GKE

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**FIGURE 52**

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT  
GCCCCGCGCCCAGTCA**ATG**ACCCTGCGCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCT  
GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA  
CCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA  
GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT  
GACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA  
GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT  
GGAAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT  
GATTGACTAATCCGAGCCAATACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAG  
GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT  
AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAA**TA**  
**A**TAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA



**FIGURE 53**

MTLRPSLLPLHLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGLTLHI  
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF  
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS  
KKKLKEEKRNKSXXX

**FIGURE 54**

CCCGGGAACGTGTTCCCTGGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCCGGCTCCCTGC  
CCCGCGCCCAGTCATGACCCTGCGCCCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC  
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC  
CTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGAGA  
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA  
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT  
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTATGG  
AAAACGGGGATTTCCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA  
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG  
ATGGCCATGGTGCCACCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA  
CCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA  
AATAATAAATTTTAAAAAACTTA

**FIGURE 55**

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCCAGAACCATGTGCC  
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG  
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA  
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT  
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT  
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG  
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC  
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA  
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAAA

[illegible][illegible]

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**FIGURE 57**

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDAAVIYPTMKDFNHSYHACGVI  
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK  
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

034439.03201  
T0320.26450

**FIGURE 58**

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGGCGGACACCGGGCTCCGGAACC  
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG  
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC  
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT  
TTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGC  
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG  
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG  
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATT  
TTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

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**FIGURE 59**

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTTCAGAATGCATGAC  
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG  
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC  
ATGCCTGTGGTGTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA  
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCTTTT  
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT  
ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC  
ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

**FIGURE 60**

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT  
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT  
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT  
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC  
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT  
GTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT  
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT  
ACCCTGGAATTNCTNTATTTTTTCCAGAATGCC



**FIGURE 61**

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC  
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT  
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC  
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG  
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN  
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC  
CCTGT

**FIGURE 62**

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCCGGCGCGG  
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAATGTTTG  
GATTTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATT  
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT  
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTATAGCAACCA  
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA  
GGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG  
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG  
TATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

**FIGURE 63**

CGACGCCGGCGTG**ATG**TGGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGGCCGTCC  
TCTGCAAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTC  
AAACGGCCCCCAGCGCCCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGC  
TTTTTCAGCCAACCAAGTGCCGGAGAAGCTGGATGTGGTGGTAATTGGCAGTGGCTTTGGGG  
GCCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCCTGGTGCTGGAACAACAT  
ACCAAGGCAGGGGGCTGCTGTCATACCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAAT  
CCATTACATTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTTATCTTGGACCAGATCACTG  
AAGGGCAGCTGGACTGGGCTCCCCTGTCCTCTCCTTTTGACATCATGGTACTGGAAGGGCCC  
AATGGCCGAAAGGAGTACCCCATGTACAGTGGAGAGAAAGCCTACATTCAGGGCCTCAAGGA  
GAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA  
GTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTGCCCCGTGGTTCAGCTCCTCGAC  
AGGTGTGGGCTGCTGACTCGTTTTCTCTCCATTCCCTTCAAGCATCCACCCAGAGCCTGGCTGA  
GGTCTGTCAGCAGCTGGGGGCCCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCA  
CTTACGGTGTCAACCCCAACCACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTAC  
ATGAAAGGAGGGCTTTTATCCCCGAGGGGGTTCAGTGAAATTCCTTCCACACCATCCCTGT  
GATTACAGCGGGCTGGGGGCGCTGTCCTCACAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT  
CAGCTGGGAAAGCCTGTGGTGTGAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTGC  
CCCATCGTGGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC  
CCGCTGCCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGCGGCCCCGGCTTAGGCATGACCT  
CTGTTTTTCATCTGCCCTGCGAGGCACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTAT  
GTTTACTATGACACGGACATGGACCAGGCGATGGAGCGCTACGTCTCCATGCCCAGGGAAGA  
GGCTGCGGAACACATCCCTCTTCTCTTCTCGCTTTCCCATCAGCCAAAGATCCGACCTGGG  
AGGACCGATTCCCAGGCCGGTCCACCATGATCATGCTCATACCCACTGCCTACGAGTGGTTT  
GAGGAGTGGCAGGCGGAGCTGAAGGGAAGCGGGGCAGTGACTATGAGACCTTCAAAAACCTC  
CTTTGTGGAAGCCTCTATGTGTCAGTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGG  
AGAGTGTGACTGCAGGATCCCCACTCACCAACCAGTTCTATCTGGCTGCTCCCCGAGGTGCC  
TGCTACGGGGCTGACCATGACCTGGGCCCGCTGCACCCCTTGTGTGATGGCCTCCTTGAGGGC  
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTGTGGACTGGTCTG  
GGGCCCTGCAAGGTGCCCTGCTGTGTCAGCAGCGCCATCCTGAAGCGGAACCTTGACTCAGAC  
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAAT**TAG**TTCCATCAGGGAGG  
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG  
CATTAGTTCCTTGACGTATAAAGCACTCTAATTTGGTTCTGATGCCTGAAGAGAGGCCTAG  
TTTAAATCACAATTCGGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA  
TCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG  
TCTCATGACGAGCGGCGCTCTGCATCCCTCACCCATGCCTCCTAACTCAGTGATCAAAGCGA  
ATATTCCATCTGTGGATAGAACCCCTGGCAGTGTGTGTCAGCTCAACCTGGTGGGTTCAAGTTC  
TGTCCTGAGGCTTCTGCTCTCATTCATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG  
GAAAAGGGAGACTAATGAGGCTTAACCTCAAACCTGGGCGTGGTTTTGGTTGCCATTCATA  
GGTTTGGAGAGCTCTAGATCTCTTTGTGCTGGGTTCAAGTGGCTCTTCAAGGGGACAGGAAAT  
GCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGTTAGTA  
GGGTGCATGTGAGATGATCATATCCAATTCATATGGAAGTCCCGGTCTGTCTTCTTATCA  
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGC  
CTTATCCACCAAATACACAGGGGAAGGGTGATGCAGGGAAGGGTGACATCAGGAGTCAGGGCA  
CACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAGTCACATCAGAAAAGGGA  
AAGCCACGGAATGTGTGTGAAGCCCAGAAATGGCATTGTGAGTTAATTAGCACATGTGAGGG  
TTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGTCTTTG  
GTATCAGACATACGAAAGGTCTCTTTGTAGTTTCGTGTTAATGTAACATTAATAAATTTATTG  
ATTCCATTGCTTTAAAAA

**FIGURE 64**

MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKEARKKVLKQAFSAN  
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG  
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ  
EEAIIIDKYIKLVKVVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ  
LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA  
GGAVLTkATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLP  
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYYDTDMDQAMERYVSMPREEAAEH  
IPLLEFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAELKGKRGSDYETFKNSFVEA  
SMSVVLKLFPPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI  
PNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLDSRIRAQKKKN

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**FIGURE 65**

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCTA  
 GGGGTTGGCACCGGCCCCGAGAGGAGG**ATG**CGGGTCCGGATAGGGCTGACGCTGCTGCTGTG  
 TGGGTGCTGCTGAGCTTGGCCTCGGCGTCCTCGGATGAAGAAGGCAGCCAGGATGAATCCT  
 TAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTAAAGGACCATACTACTGCAGGCAGA  
 GTAGTTGCTGGTCAAATATTTCTTGATTCAGAAGAATCTGAATTAGAATCCTCTATTCAAGA  
 AGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAGAAGATATCAGCTTTCTAG  
 AGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTACGGAAACCAGCTTTG  
 ACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCTTTTCTAGATAA  
 GGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTGCTACAACCT  
 ATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAACTGAAGAAGAGGCTGCTAAGAGA  
 CGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAGCAA  
 TAAGAAAAGCCAAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
 CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATC  
 CAGGCAGCGAGAGAGATGTTTGAGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGC  
 TCTTGGCTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAAGGCTCTTGTAT  
 ATTATACATTTGGAGCTCTTGGGGGCAATCTAATAGCCACATGGTTTTGGTAAGTAGACTT  
**TAG**TGGAAGGCTAATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACCTTTT  
 TCAGCTTTTCATGATCCAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACTTCCTTCAA  
 ATTCTTGTTAATGGATATAACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACA  
 ATTTTTCTTTAAATGATTAGTTTGGCTGATTGCCCCATAAAAGAGAGATCTGATAAATGGC  
 TCTTTTTAAATTTTCTCTGAGTTGGAATTGTCAGAATCATTTTTTTACATTAGATTATCATAA  
 TTTTAAAAATTTTTCTTTAGTTTTTCAAATTTTGTAAATGGTGGCTATAGAAAAACAACAT  
 GAAATATTATACAATATTTTGCAACAATGCCCTAAGAATTGTTAAATTCATGGAGTTATTT  
 GTGCAGAATGACTCCAGAGAGCTCTACTTTCTGTTTTTTACTTTTCATGATTGGCTGTCTTC  
 CCATTTATTCTGGTCATTTATTGCTAGTGACACTGTGCCTGCTTCCAGTAGTCTCATTTTTCC  
 CTATTTTGCTAATTTGTTACTTTTTCTTTGCTAATTTGGAAGATTAACATTTTTTAATAAA  
 ATTATGTCTAAGATTAAAAA  
 AA

**FIGURE 66**

MRVRIGLTLLLCVLLSLASASSDEEGSQDESLDSKTTLTSDSVKDHTTAGRVVAGQIFLD  
SESELESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG  
EPCHFPPFLFDKEYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEAAKRRQMQEAMM  
YQTGMKILNGSNKKSQKREAYRYLQKAASMNHTKALERVSYALLFGDYLPQNIQAAREMF EK  
LTEEGSPKGQTALGFLYASGLGVNSSQAKALVYYTFGALGGNLI AHMVLVSRL

**FIGURE 67**

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT  
GCCTCCCTGCCTCTGGCC**ATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT  
GTCAGTTTCCCAGACAGTCCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG  
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCCTGG  
TACCAGCAGCGGGCAGGCAGTGCCCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA  
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCCACAATGCCT  
GTGTCCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC  
TACGGCTTTAGTCCC**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTTCT  
GCCCCTGACCTTGGGTCCCTTTTAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAAATGGG  
TTAATAATATTCAACATGTCAACAAC

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**FIGURE 68**

MACRCLSFLLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG  
SAPRYLLYRSEEDHHRPADIPDRFSAKDEAHNACVLTISPVPEDDADYYCSVGYGFS

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**FIGURE 69**

GCCGCCCCGCCCCGAGACCGGGCCCCGGGGGCGCGGGGCGGGCGGGATGCGGGCGCCCCGGGGCGG  
 CGATGACCGCGGAGCGCACGCCGCGGGCCCCGGCCCTGACCCCCGCGCCCCGCTGAGCCCC  
 CCGCGCGAGGTCCGGACAGGCCGAG**ATG**ACGCCGAGCCCCCTGTTGCTGCTCCTGCTGCCCGC  
 CGTGCTGCTGGGGGCTTCCACCGGCCGCGCCCGCCGAGGCCCCCAAAGATGGCGGAC  
 AAGGTGGTCCACGGCAGGTGGCCCCGGCTGGGCGCACTGTGCGGCTGCAGTGGCCAGTGGGA  
 GGGGACCCGCGCCGCTGACCATGTGGACCAAGGATGGCCGCACCATCCACAGCGGCTGGA  
 GCCGCTTCCGCGTGCTGCCGCAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCCGGC  
 GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCCTGAGCGTCAACTACACCCTCGTCGT  
 GCTGGATGACATTAGCCCAGGGAAGGAGAGCCTGGGGCCCGACAGCTCCTCTGGGGGTCAAG  
 AGGACCCCGCCAGCCAGCAGTGGGCACGACCGCGCTTCACACAGCCCTCCAAGATGAGGCGC  
 CGGGTGATCGCACGGCCCCGTGGGTAGCTCCGTGCGGCTCAAGTGCGTGGCCAGCGGGCACCC  
 TCGGCCCCGACATCACGTGGATGAAGGACGACAGGCCCTTGACGCGCCAGAGGCCGCTGAGC  
 CCAGGAAGAAGAAGTGGACACTGAGCCTGAAGAACCTGCGGCCGAGGACGCGCAATAC  
 ACCTGCCGCTGTGCAACCGCGCGGGCGCCATCAACGCCACCTACAAGGTGGATGTGATCCA  
 GCGGACCCGTTCCAAGCCCGTGCTCACAGGCACGCACCCCGTGAACACGACGGTGGACTTCG  
 GGGGACCACGTCTTCCAGTGCAAGGTGCGCAGCGACGTGAAGCCGGTGATCCAGTGGCTG  
 AAGCGCGTGAGTACGGCGCCGAGGGCCGCCACAACCTCCACCATCGATGTGGGCGGCCAGAA  
 GTTTGTGGTGCTGCCCCGCGGTGACGTGTGGTGCAGGCCCCGACGGCTCCTACCTCAATAAGC  
 TGCTCATCACCCGTGCCCGCCAGGACGATGCGGGCATGTACATCTGCCTTGCGCCAAACACC  
 ATGGGCTACAGCTTCGCGACGCGCTTCCTCACCGTGCTGCCAGACCCAAAACCGCCAGGGCC  
 ACCTGTGGCCTCCTCGTCTCGGCCACTAGCCTGCCGTGGCCCGTGGTTCATCGGCATCCCAG  
 CCGGCGCTGTCTTCATCCTGGGCACCCCTGCTCCTGTGGCTTTGCCAGGCCCAGAAGAAGCCG  
 TGCACCCCCGCGCTGCCCTTCCCTGCCTGGGCACCGCCCCGCGGGGACGCCCCGCGACCG  
 CAGCGAGACAAGGACCTTCCCTCGTTGGCCGCGCTCAGCGCTGGCCCTGGTGTGGGGCTGT  
 GTGAGGAGCATGGGTCTCCGGCAGCCCCCAGCACTTACTGGGCCAGGCCAGTTGCTGGC  
 CCTAAGTTGTACCCCAAACCTCTACACAGACATCCACACACACACACACACTCTCACAC  
 ACACTCACACGTGGAGGGCAAGGTCCACCAGCACATCCACTATCAGTGT**TAG**ACGGCACCCGT  
 ATCTGCAGTGGGCACGGGGGGGCGGCCAGAGGAGAGCTGGGAGGATGGAGGACGGAGCT  
 GCAGACGAAGGCAGGGGACCCATGGCGAGGAGGAATGGCCAGCACCCAGGAGTCTGTGTG  
 TGAGGCATAGCCCCCTGGACACACACACACAGACACACACTACCTGGATGCATGTATGCAC  
 ACACATGCGCGCACACGTGCTCCCTGAAGGCACACGTACGCACACGCACATGCACAGATATG  
 CCGCCTGGGCACACAGATAAGCTGCCCAAATGCACGCACACGCACAGAGACATGCCAGAACA  
 TACAAGGACATGCTGCCTGAACATAACACACGCACACCCATGCGCAGATGTGCTGCCTGGACA  
 CACACACACACAGGATATGCTGTCTGGACGCACACACAGTGCAGATATGGTATCCGGACACA  
 CACGTGCACAGATATGCTGCCTGGACACACAGATAATGCTGCCTTGACACACACATGCACGG  
 ATATTGCCTGGACACACACACACACACACGCGTGCACAGATATGCTGTCTGGACACGCACAC  
 ACATGCAGATATGCTGCCTGGACACACACTTCCAGACACACGTGCACAGGCGCAGATATGCT  
 GCCTGGACACACGCAGATATGCTGTCTAGTCACACACACACGCAGACATGCTGTCCGGACAC  
 ACACACGCATGCACAGATATGCTGTCCGGACACACACACGCACGCAGATATGCTGCCTGGAC  
 ACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGATATTGCCTGGACACACACA  
 TGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATATGCTGTCCGGATACACACG  
 CACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGACACACATGCACACACAGGT  
 GCAGATATGCTGCCTGGACACACACAGATAATGCTGCCTCAACACTCACACACGTGCAGATA  
 TATTGCCCTGGACACACACATGTGCACAGATATGCTGTCTGGACATGCACACACGTGCAGATA  
 TGCTGTCCGGATACACACGCACGCACACATGCAGATATGCTGCCTGGGCACACACTTCCGGA  
 CACACATGCACACACAGGTGCAGATATGCTGCCTGGACACACGCAGACTGACGTGCTTTTGG  
 GAGGGTGTGCCGTGAAGCCTGCAGTACGTGTGCCGTGAGGCTCATAGTTGATGAGGGACTTT  
 CCCTGCTCCACCGTCACTCCCCAACTCTGCCCCCTCTGTCCCCGCTCAGTCCCCGCTC  
 CATCCCCGCTCTGTCCCCCTGGCCTTGCGCGCTATTTTTGCCACCTGCCTTGGGTGCCCAGG  
 AGTCCCCTACTGCTGTGGGCTGGGGTTGGGGGCACAGCAGCCCCAAGCCTGAGAGGCTGGAG  
 CCCATGGCTAGTGGCTCATCCCCAGTGCATTCTCCCCCTGACACAGAGAAGGGGCCCTTGGA  
 TTTATATTTAAGAAATGAAGATAATATTAATAATGATGGAAGGAAGACTGGGTTCAGGGAC  
 GTGGTCTCTCCTGGGGCCCCGGGACCCCGCTGGTCTTTAGCCATGCTGATGACCAACCCC  
 GTCCAGGCCAGACACACCCCCCAGCCCTGCTGCTGGTGGCCCCAGATCTCTGTAATTTTA  
 TGTAGAGTTTGAGCTGAAGCCCCGTATATTTAATTTATTTTGTAAACACAAAA

**FIGURE 70**

MTPSPLLLLLLPLLLLGAFPPAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM  
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDDISPGK  
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDITWMK  
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTRSKPVL  
TGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD  
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA  
TSLPWPVVIGIPAGAVFILGTL LLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPS  
LAALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTHSHTHSHVEGKV  
HQHIHYQC

**FIGURE 71**

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAACTTCCCAGGGGACCGCATTCCAGAGTC  
 AGTGACTCTGTGAAGCACCCACATCTACCTCTTGCCACGTTCCCACGGGCTTGGGGGAAAAG**AT**GGTGGGGACCA  
 AGGCTGGGTGTTCTCCTTCTGGTCTGGAAGTCACTCTGTGTTGGGGAGACAGACGATGCTCAGCCAGTCA  
 GTAAGAAGAGTCCAGCCTGGGAAGAAGAACCCAGCATCTTGGCAAGCCTGCCGACACCCTGGAGAGCCCTGG  
 TGAGTGGACAACATGGTTCAACATCGACTACCCAGGCGGAAGGGCGACTATGAGCGGCTGGACGCCATTGCT  
 TCTACTATGGGGACCGTGTATGTGCCCGTCCCCTGCGGCTAGAGGCTCGGACCACTGACTGGACACCTGCCGGC  
 AGCACTGGCCAGGTGGTCCATGGTAGTCCCGTGAGGGTCTTCTGGTGCCCTCAACAGGGAGCAGCGGCTGGCCA  
 GAAGTGTCTAATTACACCGTACGCTTCCCTGCCCCACAGGATCCCTGCGCCGAGACACAGAGCGCATCTGGA  
 GCCCATGGTCTCCCTGGAGCAAGTGCTCAGCTGCCCTGTGGTCAGACTGGGGTCCAGACTCGCACACGCATTTGC  
 TTGGCAGAGATGGTGTGCTGTGCACTGAGGCCAGCGAAGAGGGTCAGCACTGCATGGGCCAGGACTGTACAGC  
 CTGTGACCTGACCTGCCAATGGGCCAGGTGAATGCTGACTGTGATGCCTGCATGTGCCAGGACTTCATGCTTC  
 ATGGGGCTGTCTCCCTTCCCGGAGGTGCCCCAGCCTCAGGGGCTGCTATCTACCTCCTGACCAAGACGCCGAAG  
 CTGCTGACCCAGACAGACAGTGTGGGAGATTCCGAATCCCTGGCTTGTGCCCTGATGGCAAAAGCATCTGAA  
 GATCACAAAGGTCAAGTTTGCCCCATTGTACTACAATGCCAAGACTAGCCTGAAGGCAGCCACCATCAAGG  
 CAGAGTTTGAGGGCAGAGACTCCATACATGGTGATGAACCTGAGACAAAAGCACGGAGAGCTGGGCAGAGC  
 GTGTCTCTGTGCTGTAAAGGCCACAGGGAAGGCCAGGCAGACAAAGTATTTTGGTATCATAATGACACATTGCT  
 GGATCCTTCCCTCTACAAGCATGAGAGCAAGCTGGTGCTGAGGAACTGCAGCAGCAGGCTGGGGAGTACT  
 TTTGCAAGGCCCAGAGTGATGCTGGGGCTGTGAAGTCCAAGGTTGCCAGCTGATTGTACAGCATCTGATGAG  
 ACTCCTTGCAACCCAGTTTCTGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTGAGAATGCCACCAACTC  
 CTTCTACTACTGACGTGGGACGCTGCCCTGTTAAGACTTGTGAGGGCAGCAGGATAATGGGATCAGGTGCCGTG  
 ATGCTGTGCAAGTGTCTGTGGCATCTCCAAGACAGAGGAAAGGAGATCCAGTGCAGTGGCTACACGCTACCC  
 ACCAAGGTGGCCAAAGGAGTGCAGCTGCCAGCGGTGTACGGAACCTCGGAGCATCGTGCGGGGCGGTGTGAGTGC  
 TGCTGACAATGGGGAGCCCATGCGCTTTGGCCATGTGTACATGGGGAACAGCCGTGTAAGCATGACTGGCTACA  
 AGGGCCTTTTACCCTCCATGTCCCCCAGGACACTGAGAGGCTGGTGCTCACATTTGTGGACAGGCTGCAGAAG  
 TTTGTCAACACCACCAAGTGTACCTTTCAACAAGAAAGGGGAGTGCCGTGTTCCATGAAATCAAGATGCTTCG  
 TCGGAAAGAGCCCATCACTTTGGAAGCCATGGAGACCAACATCATCCCCCTGGGGGAAGTGTTGGTGAAGACC  
 CCATGGCTGAAGTGGAGATTCCATCCAGGAGTTTCTACAGGCAGAATGGGGAGCCCTACATAGGAAAAGTGAAG  
 GCCAGTGTGACCTTCCCTGGATCCCCGGAATATTTCCACAGCCACAGCTGCCAGACTGACCTGAACCTCATCAA  
 TGACGAAGGAGACACTTTCCCCCTTCGGACGTATGGCATGTCTCTGTGGACTTCAGAGATGAGGTCACTCAG  
 AGCCACTTAATGCTGGCAAAGTGAAGGTCCACCTTGACTCGACCCAGGTCAAGATGCCAGAGCACATATCCACA  
 GTGAACTCTGGTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAAGGTGATTTCAAATTTGAAAATCAAAG  
 GAGGAACAAAAGAGAAGACAGAACCCTTCTGGTGGGCAACCTGGAGATTCTGTGAGAGGAGGCTCTTTAACTGG  
 ATGTTCTCTGAAAGCAGGCGGTGCTTTGTAAAGGTGAGGGCTACCGGAGTGAGAGGTTCTTGCCTAGTGAGCAG  
 ATCCAGGGGGTGTGTATCTCCGTGATTAACCTGGAGCCTAGAAGTGGCTTCTTGTCCAACCCTAGGGCCTGGGG  
 CCGCTTTGACAGTGTATCACAGGCCCAACGGGGCTGTGTGCTGCTGCTTCTGTGATGACCACTGCCCTGATG  
 CCTACTCTGCCTATGTCTTGGCAAGCCTGGCTGGGGAGGAAGTGAAGCAGTGGAGTCTTCTCTAAATTCAC  
 CCAATGCAATTTGGCGTCCCTCAGCCCTATCTCAACAAGCTCAACTACCGTCCGACGGACCATGAGGATCCAG  
 GGTTAAAAAGACAGCTTTCCAGATTAGCATGGCCAAAGCAAGGCCCAACTCAGCTGAGGAGAGCAATGGGCCA  
 TCTATGCCTTTGAGAACCTCCGGGCATGTGAAGAGGCACACCCAGTGCAGCCCACTTCCGGTTCTACCAGATT  
 GAGGGGGATCGATATGACTACAACACAGTCCCTTCAACGAAGATGACCCTATGAGCTGGACTGAAGACTATCT  
 GGCATGGTGGCCAAAGCCGATGGAATTCAGGGCCTGTATATCAAGGTGAAGATTGTGGGGCCACTGGGAAGTGA  
 ATGTGCGATCCCGCAACATGGGGGGCACTCATCGGCGGACAGTGGGGAAGCTGTATGGAATCCGAGATGTGAGG  
 AGCACTCGGGACAGGGACAGCCCAATGTCTCAGCTGCCTGTCTGGAGTTCAAGTGCAGTGGGATGCTCTATGA  
 TCAGGACCGTGTGGACCGCACCTGGTGAAGGTCACTCCCCAGGGCAGCTGCCGTGAGCCAGTGTGAACCCCA  
 TGCTGCATGAGTACCTGGTCAACCACTTGCCACTTGCACTCAACAACGACACCAAGTGAATACCATGCTGGCA  
 CCCTTGGACCCACTGGGCCACAACATATGGCATCTACACTGTCACTGACCAGGACCCCTCGCACGGCCAAAGGAGT  
 CCAGGGTGGAGTGGTGGCTCTCTGAGATTTCCCTAGAGTTGCTCAACAGCCCCGATCAACT**TA**AGTTTGTGGT  
 ACTTCACCCTCTTCTGCCCTCATTTTGTGACAGCCATTGTGAGACTGATGCACAACTGTCACTTGGTTAAT  
 TTAAGCACTTCTGTTTTCGIGAATTTGCTTGTGTTTCTTCTCATGCCCTTACTTACTTTTCCATGCTACTGA  
 TTGGCAGTGGCCCCCAATGGCACAATAAAGCCCCCTTGTGAAACTGTTCTTTAAATGAAACACAAGAAATTT  
 GGCCACTGGTAAACTCTGCAGCTTCAACTGTACTTCAATTAATGCCATTAATGCAAAATATACTTCTCTTCTT  
 TTTGCATGGTTTTGGCCACCTCTGCAATAGTGATAATCTGATGCTGAAGATCAAATAACCAATATAAAGCATAT  
 TTCTTGGCCTTGTCCACAGGACATAGGCAAGCCTTGATCATAGTTTACATATATAAATGGTGGTGAATAAAG  
 AAATAAAACACAATACTTTTACTTGAATGTAATAAATTTATTTTCTTTGCTAAATTTGGAATTTCTAGTGC  
 ACATTCAAAGTTAAGCTATTAATATAGGGTGATCATAGTTCTCTTACCAAGTCTGGAAGAACATCTCCTGGT  
 ATCCACAATTAACCCAGGTTGCTAACTGATTTGTACATTTCCCTTTGCATTGCTTTTGTCTTGTCTAGAAAC  
 CCAGTGTAGCCAGGGCAGATGTCAATAAATGCATACTCTGTATTTGAAAAA

**FIGURE 72**

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI  
DYPGGKGDYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPREGFWCLNREQ  
RPGQNCNSNYTVRFLCPPGSLRRDTERIWSPWSPWSKCSAACGQTGVQTRTRICLAEMVSLCS  
EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK  
TPKLLTQTDSDGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY  
MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQQHQAG  
EYFCKAQSDAGAVKSKVAQLIVTASDETPCNPVPESYLIRLPHDCFQONATNSFYDVGRCPV  
KTCAGQQDNGIRCRDAVQNCCGISKTEEREIQCSGYTLPTKVAKESCQRCTETRIVRGRV  
SAADNGEPMRFHGVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLPFN  
KKGSASFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPYIGKV  
KASVTFLDPRNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL  
DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKRDRFTLVGNLEIRERRLFNL  
DVPESRRRCFVKVRAYRSEFLPSEQIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA  
CVPAFCDDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRRTDHEDPR  
VKKTAFQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDYNTVPFN  
EDDPMSWTEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS  
TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTL VKVIPQGSCRRASVNPMLEHYLVNHLPLAV  
NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTS DGSSRIMKSNVGVALT  
FNCVERQVGRQSAFQYLQSTPAQSPAAGTVQGRVPSRRQQRASRGGQRQGGVVASLRFPRVA  
QQPLIN

**FIGURE 73**

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC  
AATATCTTAACTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG  
ACCTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACTAGACAAAGATCGCAGATCATAAAGC  
AAGCTCTGCTTTAGTTTTCCAAGAAGATTACAAAGAATTTAGAGATGTTATTTGTCAAGATCCCTGTGATTTCATG  
CCCTTTGGGTACGGTGTCTCAGTGATGCAGCCCTACCCTTTGGTTTGGGGACATTATGATTTGTGTAAGACT  
CAGATTTACACGGAAGAAGGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATA  
TCTGAAAGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCTCCTGAGACGTTCTGTGCAATGGGCAATC  
CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGATTTT  
GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGGGAAGGAGTATCCCAAGCCTCTCCAGGTTAACAT  
CACTCTGTCTTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC  
AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA  
GATGCTTTTTCATATGGATCCTAAATCCGTGAAGGATTTATCACAGCATACGGTCTTAGAAATCATTTGCACAGA  
AGAGTACTCAACAGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTCCGCGCTTTTGTG  
CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT  
ACAGTCACAGACCTGAGGATAAGGCTGTTAAGACCAGCCGTGGGGAAATATTTGTAGATGAGCTACACTTGGC  
ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAATCTCCATGCCACTGTATGTG  
TGTATGACAACAGCAAAATTGACATGCGAATGTGAGCACAACTACAGGTCCAGACTGTGGGAAATGCAAGAAG  
AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCACTGCAAAATACCTGTATCCC  
CAGTATTTCCAGTATTGGTACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGACGTGCCACA  
ACAACGTGCGCTGCCTGTGCCCCGGCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGTGGC  
AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCCCGCACGGCACCCCGAGCGCTGCTGCTGTGACCACGCTGCT  
GGGAACCGCCAGCCCCCTGGTGTCTTAGGTGTACCTCCAGCCACACCGGACGGGCTGTGCCGTGGGGAAGCA  
GACACAACCCAAACATTTGCTACTAACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAA  
CTAAGAAGGCCTAACTGAACCTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTT  
TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAATCACATTGCCAGCTGCAGAGCATATTGTGGA  
TTGGAAAGGCTGCGACAGCCCCCAAACAGGAAAGACAAAAACAAACAAATCAACCGACCTAAAAACATTGGC  
TACTCTAGCGTGGTGCGCCCTAGTACGACTCCGCCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAG  
GTGCTTTGTGGGCATAAGGAAATCTGTTACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAAC  
CTGTGCTTTTAGTGAACGTTGCTCTGTAACCCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACA  
TGTGTAACAGCCCCCTCTAAAAGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA  
GCACACACCCACTATACAAGAGTGGCTATAGGAAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTT  
ATTTTTCTTGAACCTACTGTAATATGTAGATTTTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAAT  
GTATCTAATTCGAATCAGCAAAGACTGACATTTTATTTTGTCTCTTTTCTGTTTGTGTTTCACTGTGCAGA  
GATTTCTCTGTAAGGGCAACGAACGTGCTGGCATCAAAGAATATCAGTTTACATATATAACAAGTGTAATAAGA  
TTCCACCAAAGGACATTCTAAATGTTTTCTTGTGCTTTAACACTGGAAGATTTAAAGAATAAAAACTCCTGCA  
TAAACGATTTTCAAGGAATTTGTATTGCAATTTCTTAAGATGAAAGGAACAGCCACCAAGCAGTTTCACTCACT  
TTACTGATTTCTGTGTGGACTGAGTACATTGAGCTGACGAATTTAGTTCCCAGGAAGATGGATTGATGTTCACT  
AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAA  
AAAAAA

**FIGURE 74**

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK  
VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPPELMFDFEGRHPSTFWQSATWK  
EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF  
HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEIKDRFALFAGPRLRNMASLYGQLD  
TTKKLRDFFTVDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN  
SKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGTANTCIPSISSIGTNVCDNELLH  
CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTAS  
PLVF

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**FIGURE 75**

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCCGGCTAAGATTGCTGAGGAGGCGG  
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCGGTCCGGGCGAGGTGTCCTCATGACTT  
 CTCTTGTGGACC**ATG**TCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCC  
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA  
 AGAGTTTAGCCTTGCGACTGGCCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT  
 AGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC  
 AGCAGCCATGGCCTTCTGCTTCCTGGAGACCTGTGGTGGGAATTCACAGCTTCCTATGACA  
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAG  
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGA AAAAAT  
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA  
 ATGGGGTGATGAATGGTCACACACCGATGCACCTGGAGCCTGCTCCTAATTTCCGAATGGAA  
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCT  
 CATTCGAGGAGTTACCTTGCGA AACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT  
 TGGACCAAACCTCG**TGA**GCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT  
 CCGGGAGCAGTGATGTCAA ACTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA  
 AAAGGGCATGTGAGTGA AATCTGGGAATGGCTGGATTTCGGAAACATCTGCCCATGTGTATTG  
 ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTTAGGGTAAAATTAACAAATCCATTCTAT  
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTT  
 GCTTCAGAAGTGTTATTTTCATGAATCATTCATATGATTTGATCCCCCAGGATTCTATTTTGT  
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCAT  
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTCATGTTACACAAGCTTCTTACGGTTTTTC  
 TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAAACTCAGTAGTACAACC  
 TAAACTTGATAAAAAGTGTTGTA AAAATGTATAGCCATTTATATCCTATGTATAAATTAATG  
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAAAAA AAAAAAAAAAAAAA  
 AAAAG

**FIGURE 76**

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF  
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW  
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA  
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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**FIGURE 77**

TGCTTCCTGGAGACCCCTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT  
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATT  
TTAACTATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAG  
TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAATGGGGT

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**FIGURE 78**

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA  
 CCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAAACGAGGCGGGTGGTG  
 CCTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT  
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCTT  
 CCTCCCCGCTCGTCCCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA  
**TG**GGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC  
 GAGTGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGAC  
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA  
 TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTCTGCTCCTGCCC  
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCTCGGAACTACTACATCCAGTGGCT  
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA  
 TCTTCCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG  
 GGTGTCTTGGGCCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT  
 AGGTATGGTGTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT  
 ATGACTTTTGGGAGTACTATCTCCCCTACCTCTACTCATGCATCTCCTTCTTGGGGTTCTG  
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT  
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG  
 CAGCCCTGACCCGCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCTTTAGACATGGAGCTG  
 CTACACAGACAGGTCCTGGCTCTGCAGACACAGAGGGTCCTGCTGGAGAAGAGGCGGAAGGC  
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGCTGGTGCTGACGG  
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG  
 CCCCAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG  
 TGCCGTCAATCAGGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTATA  
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATT  
 GGGAACTGTGTCTGTCTCCTGGTCCCTAAGCTCAGCACTTCTGTCTTCTCTCGAACCTGGG  
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA  
 TTGTGTTCTCTACAACGCAGCCTTTGCAGGCCTCACCACACTCTGTCTGGTGAAGACCTTC  
 ACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCTTTGGGCTGGACAGACTGCCGCTGCCCCGT  
 CTCCGGTTTCCCCCAGGCATCTAGGAAGACCCAGCACCAGTGAACCTCCAGCTGGGGGTGGGA  
 AGGAAAAAACTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGG  
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATT  
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAAGTGTGGCCT  
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCCTGATCCCAAATCTGTTTACACATCA  
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTTGATGTGCAAT  
 AGGGTGGGGTAGGGGACAGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCC  
 CTTGCCTCTGGCCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTG  
 AAAGACCAAGGGGATAGGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCCAGGGA  
 AAAAAA

**FIGURE 79**

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK  
IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGSLIHGLWNLVFLFPNLSL  
IFLMPFAYFFTESEGFAGSRKGV LGRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL  
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEEQLYCSAFEE  
AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT  
GLSVLIVAIHILELLIDEAAMPGRMQGTS LGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGFY  
SSPLFRSLRPRWHD TAMTQIIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY  
IVFLYNAAFAGLTTLC LVKTFTA AVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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**FIGURE 80**

GGCTGCCGAGGGAAGGCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC  
GCTCGTCCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC  
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA  
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC  
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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**FIGURE 81**

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAAACGAGGCGGTGGTGC  
CTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC  
TGTCGCAGGCTGCGAGGAAAGGCCCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGCGGCTTCCT  
CCCCGTTGTCNTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA  
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT  
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC  
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC  
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCCTGCTCCTGCCCTTCT  
CCATCATCAGCAATGAGGTGCTGCACTCCC

**FIGURE 82**

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT  
GGAATTGAGGAAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTT**CATG**CTGCTGT  
GGGTGATATTACTGGTCCTGGCTCCTGTCAGTGGACAGTTTGCAAGGACACCCAGGCCCATT  
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCTCACTTGCAA  
GGGATTTTCGCTTCTACTCACCACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA  
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAGGAATCTGGAGAGTACAGATGCCAG  
GCCCAGGGCTCCCCTCTCAGTAGCCCTGTGCACTTGGATTTTTCTTCAGAGATGGGATTTCC  
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCT**TAG**GCCTCTC  
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC  
TCTGTGGTTCTGAGGTGCCGGGCAAAGGCGGAAGTAACACTGAATAATACTATTTACAAGAA  
TGATAATGTCCTGGCATTCTTAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA  
AAA

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**FIGURE 83**

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQGTKWYHRYL  
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLD FSSEM GFPHAAQANVELLGSSDLLT

0541392.03204  
T02230.25574660

**FIGURE 84**

CAGAAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCCCCGGTGT  
 GAGGCGGCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGGCGGCGGAGGAGGCTGTGAG  
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACC**ATG**GCTCCGCAGAACCTGAGCACCTTTT  
 GCCTGTTGCTGCTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG  
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTA AAAAGGCCCTATAGGAACTAGCCCTGCA  
 GCTTCATCCCGACCGGAACCCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG  
 CTGCTTATGAGGTTCTGTGATAGTGAGAAACGGAAACAGTACGATACTTATGGTGAAGAA  
 GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTCACACTTCTTTGGGGATTT  
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTCCAAGAGGAAGTGATA  
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT  
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAAACGGAAGTGCAATTGTCGGCAAGAGAT  
 GCGGACCACCCAGCTGGGCCCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT  
 GCCCTAATGTCAAACCTAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG  
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG  
 AGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT  
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT  
 CACTTGGATGGTCACAAGGTACATATTTCCCGGGATAAGATCACCAGGCCAGGAGCGAAGCT  
 ATGGAAGAAAGGGGAAGGGCTCCCCAACTTTGACAACAACAATATCAAGGGCTCTTTGATAA  
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA  
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATAT**TG**AGAGTG  
 AATAAAATTGGACTTTGTTTAAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT  
 TTGTGTGTGTTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA  
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTTCGAAAAGAATGACC  
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGCTGCCGCCTGAGT  
 TTCAAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA  
 GTTGTTAGCAATTCATTCAAAATGCCAACTGGAGAAGTCTGTTTTTAAATACATTTTGTG  
 TTATTTTTA



**FIGURE 85**

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDDPQ  
AQEKFQDLGAAYEVLSDSEKRRKQYDTYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGTTPRQQ  
DRNIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ  
MTQEVVCDECPNVKLVNEERTLEVEIEPGVVDGMEYPPFIGEGEPHVDGEPGDLRFRIKVVKH  
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD  
NNNIKGLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 254-257

**Nt-dnaJ domain signature.**

amino acids 67-87

**Homologous region to Nt-dnaJ domain proteins.**

amino acids 26-58

**N-glycosylation site.**

amino acids 5-9, 261-265

**Tyrosine kinase phosphorylation site.**

amino acids 253-260

**N-myristoylation site.**

amino acids 18-24, 31-37, 93-99, 215-221

**Amidation site.**

amino acids 164-168

**FIGURE 86**

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA  
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT  
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG  
ACGAGATTTNTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG  
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCCTGATGATCCACAAGCCCAG  
GAGAAATTCCAGGATTTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA  
GTACGATAATTATGGTGAAGAAGGATTAAAAGATGGTNATCAGAGCTCCCATGGAGACATTT  
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA  
AATATTCCAAGAG

09941992.032301

**FIGURE 87**

GGCACGAGGCGGCGGGGAGTCGCGGGATGCGCCCCGGGAGCCACAGCCTGAGGCCCTCAGGT  
CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCA  
GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**  
AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGCAGCC  
TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC  
TAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC  
TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC  
GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGAC  
AGAGAAGCTTGTTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA  
GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG  
TACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGAG  
TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACC  
AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG  
CCAGATAAAGGCCTCCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTT**TAGT**GCCT  
ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT  
CTACTTTTTCCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG  
TAAAGCAGGAGATCCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACGTGGCTGGTGAGT  
GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACCTCTCTGCAAGAGGAGTATTGAAAA  
CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCT  
AAGAAATCAAGAGGTTTCACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAATG  
TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC  
TTCTTTTGGCAAGACTTGTAATCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT  
GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGTTTGGGTTTGAAGCTGAGGAACT  
ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG  
GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

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**FIGURE 88**

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL  
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSAS  
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI  
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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T0330 266T460

**FIGURE 89**

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTCCGAGGTGCTTTCGCCGCTGTCC  
CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGA  
TTTGGAGTGTTTTTCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT  
TGGAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAGAACATTTCAGAT  
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTC  
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTCAG  
GGGCTTCTTCTGTGCTTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT  
TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACA  
AGTGAATTTGAAGACTCATTTAAATATTGTGTTATTTATAAAGTCATTTGAAGAATATTCA  
GCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTTTACAGGAGTTTAAACGTATAG  
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA  
ACTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA  
ACTCTTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA  
CTGTGGTGCCTGTTTCTTTCTTTTTATTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT  
TTTTAGAAGTGCCACTGCAATGGCAAAAATATTTCCAGTTGCACTGTATCTCTGGAAGTGA  
TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAACCAAGGAAACCCCAATTTTG  
ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

**FIGURE 90**

MISLTDTQKIGMGLTGFGVFLLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK  
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFLLFRGFFPVVVGFIIRVPVLGSLLNLPGI  
RSFVDKVGESNNMV

**Important features:**

**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

**N-myristoylation sites.**

amino acids 11-16, 51-56 and 116-121

**Aminoacyl-transfer RNA synthetases class-II protein.**

amino acids 49-59

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC  
ACCNTGGGCTTTCCGAGGTGCTTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA  
CGGACACGCAGAAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTTCTGTCTTTTGA  
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT  
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG  
CTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG  
ATCTTCGAAATTTATGGATTTTTTCTCTTGTC

**FIGURE 92**

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA  
GGCTGCCAGGAAGGAGACGCCTTCCTGAGTCCTGGATCTTTCTTCCTTCTGGAAATCTTTGA  
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**CATG**GACCTCGCGGGACTGC  
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC  
ATCAACACCATTTCAGCTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCCGGAA  
GATCAACTGCAGACTGTCCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT  
CGGGCACGGAATGCACCATCTTCACGGACCCGCGCGCCTACCTCAAGTATGGGAAGGAAAAT  
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA  
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA  
TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT  
CGCAAGACGGTTGCCACCAGTTTGCAGCACCTCCGGGACTACCCCGAGAAGTATTTTTTTCCT  
GATTCACTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC  
GGGCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC  
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTCAGAAA  
TAATGAAAATCCAACACTGCTGGGAGTCCTAAACGGAAAGAAATACCATGCAGATTTGTATG  
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC  
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCCGA  
GACGCCCATGGTGCCCCCCCCGGCGGCCCTGGACCCTCGTGAACCTGGCTGTTTTGGGCCTCGC  
TGGTGCTCTACCTTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG  
CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT  
GACGGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT**T**  
**G**ACTCAGGGAGGTGTCACCATCCGAAGGGAACCTTGGGGAACTGGTGGCCTCTGCATATCCT  
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCCTGCTGGGCACGGCGGAAGTCACGA  
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGGATGGGGAGGAAGATGTTTTGTAATCTTT  
TTTTCCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC  
TGTGTGGTGAGTGTGAACTTTGTTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG  
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCCTTTCATCCTTTGGTGCTGAGTTTTCTGT  
AACCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC  
CAAGAAAAAAAATTAAAGTGCTTTTCTGGGTCAAAAAAAAAAAAA



**FIGURE 93**

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLV  
MLEWWSGTECTIFTDPRAYLKYGKENAIVVLNHHKFEIDFLCGWSLSERFGLLGGSKVLAKK  
ELAYVPIIGMMWYFTEMVFCSRKWEQDRKTVATSLQHRLRDYPEKYFFLIHCEGTRFTEKKHE  
ISMQVARAKGLPRLKHLLPRTKGFATVRSLRNVVSAVYDCTLNFRNNENPTLLGVLNGKK  
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEYYRTGTFPETPMVPPRRPWTLVN  
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRWMIGVTEIDKGSAYGNSDS  
KQKLND

T02280" 266T460

**FIGURE 94**

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG  
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAA  
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTA  
 TACAATTGACATTCAGAAATATATTCCATGCTATCAGCTTTTATAGCTTTTATAATTCTTCAG  
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT  
 TGGTACAAATTCCGTCGTCATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA  
 AAAGTTGCAGGAGCATTTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAA  
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTT  
 TTTTACAGGGTACCTTTAGTGTTGCCAATCTGGGCATGTCTGAACAAGTGGTTATAAAAC  
 TGTATCAGGTTCCCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT  
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA  
 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACT  
 AGTAAAGGATGTAAACAGATTAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGG  
 CAGCAAGAGAGAAGAACATCCAAAAAGACCCTCAGGAGAACATTTTTCTTTGTCAGGCATTA  
 CGGACCTTTTTTCCAAATTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA  
 TGTCTTCTAAAAGTAGCTGTAACCTACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA  
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT  
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA  
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC  
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA  
 TTT**TGA**TCCTTTTTAACCTTACAAGGAGATTTTTTTATTTGGCTGATGGGTAAAGCCAAACAT  
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTAC  
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC  
 ATCAGATGCTTTTATTTCCAAACCTTTTTTTTACCTTTCACTAAGTTGTTGAGGGGAAGGCT  
 TACACAGACACATTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA  
 TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC  
 TGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAAATGGAAAAGCAAGAATAGCCTTAT  
 TTTCAAATATGGAAGAAATTTATATGAAAATTTATCTGAGTCATTAAAATTCTCCTTAAG  
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA  
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

**FIGURE 95**

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQ  
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEH  
FSNQDLVFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGKTVSGSC  
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN  
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSS  
CNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDDRWQFKRSRLLDTDKRSKA  
NTGSSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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**FIGURE 96**

GGCACAGCCGCGCGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGC  
CCAAGCAGCGCGCAGCGAAGCGCCGCGCCGCCACACCCCTCTGCGGTCCCCGCGGCGCCTGCCACCCCTTCCCT  
CCTTCCCCGCGTCCCCGCTCGCCGCGCCAGTCAGCTTGCCGGGTTGCTGCCCCGCGAACCCTCGAGGTCACCA  
GCCCCGCGCTCTGCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCCTGGCCCGCGCCTGGCACC  
GGGGACCGTTGCCTGACGCGAGGCCAGCTCTACTTTTCCCCCGCGTCTCCTCCGCTGCTCGCCTCTTCCAC  
CAACTCCAACCTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAG  
CGCCGCTTCCCGTCCGCTCCCAAAGGTGGGAACGCGTCCGCCCGCGCCGACCA**ATGG**CACGGTTCCGGCTTGCC  
CGCGCTTCTCTGCACCCTGGCAGTGCTCAGCGCCGCGTGTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGG  
AAGTGCGACGTCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCAT  
TTGAAGATCTGTCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGA  
TGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTACAGTTACAAGAAGTTTG  
ATGAATCTTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT  
TTATACATGCAAAATTTCTGAGCTATTTAAAGATCTCTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT  
GAACCTGGAAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGT  
ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCT  
CGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTGCTCAAGGCTTAGCGGTTGCGGG  
AGATGTGCTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACT  
GCTCCCACTGCCGGGCTCTCGTGACTGTGAAGCCATGTTACAACACTGCTCAAACATCATGAGAGGCTGTTTG  
GCCAACCAAGGGATCTCGATTTTGAATGGAACAATTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA  
GGGTCCCTTTCAACATTGAATCGGTGATGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG  
ATAATAGTGTTCAGTGTCTCAGAAGGTTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATT  
TCTCGTTCCATCTCTGAAAAGTGCCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCACAGC  
AGCTGGCACTAGTTTGGACCGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCCT  
CCCTCCGAGCAACGTTTGAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGG  
AAAGGCAAAAGCAGGTACCTGTTTGCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCCA  
GGTTGACACCAGCAAACCAGACATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGA  
AGAATGCATACAATGGGAACGACGTGGACTTCTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGGAAAGT  
GGCTGTGAGTATCAGCAGTGCCCTTCAGAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGA  
GAAAGCCGACAGTGCTGGTGCTCGCTCGGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGG  
TTATGCAGAGAGAGTGAGAT**TAA**TTCTCAAACCTCTGAGAAAAAGTGTTTCATCAAAAAGTTAAAAGGCACCAAGTT  
ATCACTTTTCTACCATCCTAGTGACTTTGCTTTTTTAAATGAATGGACAACAATGTACAGTTTTTACTATGTGGC  
CACTGGTTTAAAGAAGTGCTGACTTTGTTTTCTCATTCAGTTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGT  
TCCTGCTCCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAAGTATAGTTAGTTGTGCATTTGTGA  
TTTTTATCACTCTATTATTTGTTTGTATGTTTTTTTCTCATTTTCGTTTGTGGGTTTTTTTTTCCAACTGTGATCT  
CGCCTTGTCTTACAAGCAAACAGGGTCCCTTCTTGGCACGTAACATGTACGTATTTCTGAAATATTAAATA  
GCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAAGCCCCAAAAGC

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T02280.266466

**FIGURE 97**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ  
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF  
VKTYGHLYMQNSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFRLVNSQYHFTDEY  
LECVSKYTEQLKPFQDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL  
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES  
VMDPIDVKISDAIMNMQDNSVQVSQKVFQGC GPPKPLPAGRISR SISESAFSARFRPHHPEE  
RPTTAAGTSLDRLVTDVKEKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLF  
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFFDISDESSGE  
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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T0220'256T450

**FIGURE 98**

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT  
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA  
GCAACTTACAGCTGCACCGACAGTTGCG**ATG**AAAGTTCTAATCTCTTCCCTCCTCCTGTTGC  
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC  
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA  
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGC  
AGTGCCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA  
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT  
TGCTCTGCCTTTG**TAG**GAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA  
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCCACTGTACCCACC  
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGCTCTC  
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTT  
AATTACCTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTCAATTAACCTTAAATGC  
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

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**FIGURE 99**

MKVLISSLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRR  
KFMTVSGLPKKQCPCDHFKGNVKKTRHQRRHRKPNKHSRACQQFLKQCQLRSFALPL

094493 08280  
"26674600

**FIGURE 100**

A**A**TGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT  
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA  
AAGCCAGACTTCCCCAAATTCCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA  
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA  
AACATTCATCAAAG**TGA**CATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA  
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC  
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC  
CTGACTGCATTTTTGCTTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG  
ATGGAGAGGAAA



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**FIGURE 101**

MAVLVLRLTVVLGLLVLFLTCYADDKPDKPDDKPDSSGKDPKPDFPKFLSLLGTEIIENAVE  
FILRSMSRSTGFMEFDDNEGKHSSK

FOOD-284780

**FIGURE 102**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT  
 CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCCTCCTGCAGCTGCTGGTGCTGCTTCTTAC  
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCTGTGCAAAGCTACTTCC  
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG  
 CTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG  
 CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC  
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT  
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT  
 GGTGGTCTGCACTCTGGTGCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCC  
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA  
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCCACCTGGAAACACATTGGGGATGGCTG  
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCCAGTTCTCCGAAATCCAAATGG  
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC  
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA  
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACC**TAG**CAGAATGAGAGAAGACATT  
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC  
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC  
 TGTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTC  
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT  
 CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCT  
 CTCCCCACTACCACCTTCTTCCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT  
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA  
 AACCACG

**FIGURE 103**

MDILVPELLQLLVLLLTLP LHL MALLGCWQPLCKSYFPYLM AVLTPKSNRKMESKKRELF SQI  
KGLTGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVV  
APGEDMRQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRLRPGGVLFFWEHVAEPYGSWAFM  
WQQVF EPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPVGPHIMGKAVKQSFP  
SSKALICSFPSLQLEQATHQPIYLPLRGT

T08280" 266T460

**FIGURE 104**

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG  
CAGATGTTGGGGCTTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA  
ACTAATATTTATATGACAGAAGAAAAAG**ATG**TCATTCCGTAAAGTAAACATCATCATCTTGG  
TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG  
TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCCTCAACCTATAGACTTTGTCCCAA  
TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTG  
AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTTCAGCACAACTCGCTCCAAT  
GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAG  
TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCCTAACTTTTGGAAGGAA  
AAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC  
TTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA  
AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG  
AAGATTGTGATTTCAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTAC  
ATTGGCTATCTTGACTATAAAAAGGAAAGAATTCGTAAGCTTTCCATGAAAGCCAGCACTTG  
CTCATTTAATCCTGGAGTTTTTGTGTCAAACCTGACGGAATGGAAACGACAGAATATAACTA  
ACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTGGCT  
GGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC  
TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA  
AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT  
ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAACAGGCAAATTCACCTAATCCGAAG  
ATATACCGAGATCTCAAACATAAAG**TGA**AACAGAATTTGAACTGTAAGCAAGCATTTCTCAG  
GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA  
GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC  
AGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTT  
ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA  
TAATTCAAACTGCTGTTGGTTTTAATTTTGTAACCTGTGGCCTGATCTGTAAATAAACTT  
ACATTTTTC

**FIGURE 105**

MSFRKVNI I I L V L A V A L F L L V L H H N F L S L S S L L R N E V T D S G I V G P Q P I D F V P N A L R H A V D G R  
Q E E I P V V I A A S E D R L G G A I A A I N S I Q H N T R S N V I F Y I V T L N N T A D H L R S W L N S D S L K S I R Y K  
I V N F D P K L L E G K V K E D P D Q G E S M K P L T F A R F Y L P I L V P S A K K A I Y M D D D V I V Q G D I L A L Y N T  
A L K P G H A A A F S E D C D S A S T K V V I R G A G N Q Y N Y I G Y L D Y K K E R I R K L S M K A S T C S F N P G V F V A  
N L T E W K R Q N I T N Q L E K W M K L N V E E G L Y S R T L A G S I T T P P L L I V F Y Q Q H S T I D P M W N V R H L G S  
S A G K R Y S P Q F V K A A K L L H W N G H L K P W G R T A S Y T D V W E K W Y I P D P T G K F N L I R R Y T E I S N I K

**FIGURE 106**

TGGTTTTTGGCCCATAAATTCCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT  
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT  
GGGAGACAAGAGGAGATTCCCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT  
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC  
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCCTGAAAAGCATCAGA  
TACAAAATTGTCAATTTTGACCCTAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA  
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG  
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC  
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC  
TAAAGTTGTCATCCGTGGAGCAGGAAA

**FIGURE 107**

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG  
GAGCTAGAGGGCAAGTGTGCTCGGCCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC  
TGGGCTCCGGGGCCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGGCGCGGGCTGCA  
TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGCCGCGGCGAGCCTTTGAGGGGAACGACT  
TGTCGGAGCCCTAACCAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGGAGCGTCACATCACT  
TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT  
CCGTAAAGTAAACATCATCATCTTGGTCCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC  
CATAACTTCCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTCAGGAATTGTAG  
GGCCTCAACCTATAGGACTTTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA  
GGAGATTCCGTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA  
ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA  
GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG  
TCAATTTTGACCCTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC  
ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGGTTCCCAGCGCAAAGAAGG  
CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA  
CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT  
CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA  
TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC  
CTGACGGAATGGAAACGACAGAATATAACTAACCAACTGGAAAAATGGATGAACTCAATGT  
AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG  
TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGT  
GCTGGAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA  
TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATTCCA  
GACCCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA  
CAGAATTTGAACTGTAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCGTGGGAAG  
TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAG  
GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCCAGACAGACTATAGACTATAAAT  
ATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTGAATGACTGGAAAGAAGAA  
CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTAATTTT  
GTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTCAATAGGTAAAAA

**FIGURE 108**

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT  
GAAGGCCGGCCATACCAGAGTCCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG  
TCTGTGCTGGTCTGAGGGTGCTGCCTGTC**ATG**GGGGCAGCCATCTCCCAGGGGGCCCTCATC  
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTCTGGGTATCCTCTGCTG  
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC  
TGGCCCCTGTCCTGAGAAGGCCCCACCACCCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC  
TGCAGCCCTGAAGGCCCCTGGCCTAGCCTGGAGCCCAGGACC**TAA**GTCCACCTCACCTAGAG  
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT  
TGGAGCTGGACCCAGCGGCCCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC  
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT  
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC  
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG  
GCTGGGCCCCTCCCCTGGTCCTCCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA  
AAAAAAAAAAAAAAAAAAAA



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**FIGURE 109**

MGA AISQGALIAIVCNGLVGFLLLLLWVILCWACHSRLPTLTLSLNPVPTPALAPVLRPHH  
PRSPAMKAATCCSPEGPWPSLEPRT

094492 25674660

**FIGURE 110**

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCA  
GTTCCCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA  
CTCCCTATTTGCATCTGTTTTGATAAATGATGTTGACACCCTCCACCGAATTCTAAGTGGA  
TC**ATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC  
ATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT  
TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC  
TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCTATCGTA  
TCCACAGGCATCACGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT  
GACAGTTGAGCTTTTCCAAATCACAAATAAAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCC  
AGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG  
AGCCTGGGAAGTGCAGGAGCTGCCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCCCT  
TTCGGGCATTCGGTACATGTGGTCTGACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA  
TCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGT  
AAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA  
AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAGGATTCGAGAAATCATTGTCA  
TGACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA  
TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA  
TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT  
TGTTCCAAGAACTCAAGTCACCTTACATCTATTAACCTGCTTTGGAGACTTCATAATTTTTCTA  
GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG  
GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTTGCCTACTTAGTAGCCC  
ATAGTTTTTTATCTGTGTTTGAACTGTGCTGGATGCACTTTTCCTGTGTTTTGCTGTTGAT  
CTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT  
CGTAAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGA  
ATGAGGAGGGGAACAGAACTCCAGGCCATTGTGAGAT**TAG**ATACCCATTTAGGTATCTGTACCT  
GGAAACATTTTCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT  
AGTGAATTTTTTTTTTAAAAGACCTAATAAACCTATTCTTCCTCAAAA

**FIGURE 111**

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFCVGLWWLYDYTNDL  
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ  
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI  
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVM  
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDECTSAKDAFKIL  
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH  
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN  
EEGTELQAIVR

T08280"255F4550

**FIGURE 112**

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTT  
 AGAATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTG  
 TGTGGTGAAAATTTTTTGAIAAAAAAAAAATTCCTTCTTCAAACAAGGGTGTCATTCTGATATT  
**TATG**AGGACTGTTGTTCTCACTATGAAGGCATCTGTTATTGAAATGTTCCCTTGTITTTGCTGG  
 TGACTGGAGTACATTCAAACAAGAAACGGCAAAGAAGATTAAAAGGCCCAAGTTCACTGTG  
 CCTCAGATCAACTGCGATGTCAAAGCCGGAAGATCATCGATCCTGAGTTCAATTGTGAAATG  
 TCCAGCAGGATGCCAAGACCCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACT  
 CCAGTGTGTGTGGCGCTGCCGTACACAGTGGTGTGCTTGATAATTCAGGAGGGAAAAATACTT  
 GTTCGGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTT  
 ATCCCTACCACGATGGAGAGAATCCTTTATCGTCTTAGAAAAGTAAACCCAAAAAGGGTGTA  
 CCTACCCATCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGGTGAGACC  
 ACAAAGCCTATCAGAGGCCACCTATTCCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA  
 GCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCAACCTTGCCAAGGCCATCCCTTCTG  
 CTCTGTTCTACCACAGCATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT  
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAAAACAGGCCCAGAGCTGATCCAGGTATCCA  
 AAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAAACCTGTTGGAGCGGATGTGAGCCTGGGAC  
 TTGTTCCAAAAGAAGAATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC  
 TGCAAAATTGACTTGTCTGTTTTTAATTGATGGGAGCACCAAGCATTGGCAAAACGGCGATTCCG  
 AATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGCCGGTCCAC  
 TGATGGGTGTTGTCCAGTATGGAGACAACCCTGCTACTCACTTTAACCTCAAGACACACAG  
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAATGT  
 AGGTCCGGGCCATCTCCTTTGTGACCAAGAACTTCTTTTCCAAAGCCAATGGAAACAGAAGCG  
 GGGCTCCCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT  
 TCAAGACTTGCAGAGAGATCAGGAATCAACATTTTCTTCATCACCATTGAAGGTGCTGCTGA  
 AAATGAGAAGCAGTATGTGGTGGAGCCCAACTTTGCAAAACAAGGCCGTGTGCAGAACAAACG  
 GCTTCTACTCGCTCCACGTGCAGAGCTGGTTTGGCCTCCACAAGACCCCTGCAGCCTCTGGTG  
 AAGCGGGTCTGCGACACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAACCTCGGCTGACAT  
 TGGCTTCGTCTATCGACGGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCACCGTCTCCAGT  
 TTGTGACCAACCTCACCAAAGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCCGTG  
 CAGTACACCTACGAACAGCGGCTGGAGTTTGGGTTTCGACAAGTACAGCAGCAAGCCTGACAT  
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCAGCACGGGGGCTGCCATCA  
 ACTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAAGCCCAACAAGAGGAAGTTAATGATCCTC  
 ATCACCGACGGGAGGTCTACGACGACGTCCGGATCCCAGCCATGGCTGCCCATCTGAAGGG  
 AGTGATCACCTATGCGATAGGCGTTGCCTGGGCTGCCCAAGAGGAGCTAGAAGTCATTGCCA  
 CTCACCCCGCCAGAGACCACTCCTTCTTTGTGGACGAGTTTGACAACCTCCATCAGTATGTC  
 CCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTTCAGAG  
 CAGGCAGAGCACCAGCAAGTGCTGCTTTACTAACTGACGTGTTGGACCACCCACCGCTTAA  
 TGGGGCACGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAACAAATGTCTTGTTATTA  
 TTCTTTGCCATCATGCTTTTTTCATATCCAAAACCTGGAGTTACAAAGATGATCACAAACGT  
 ATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGACAATT  
 GTTTTCAAATAAATGTTCCGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTT  
 GTGAGATTTTTAAGTTGTTATTTCTGATTTGAACTCTGTAACCCTCAGCAAGTTTCATTTT  
 GTCATGACAATGTAGGAATTGCTGAATTAATGTTTAGAAGGATGAAAAATAAAAAAAAAA  
 AA  
 AAG

**FIGURE 113**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKC  
PAGCQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL  
SLPRWRESFIVLESKPKKGVITYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQ  
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTTSSQNRPRADPGIQ  
RQDPGGAFFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR  
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKTHTNLRDLKTAIEKITQRGGLSNV  
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE  
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLLQPLVKRVCDTDRACSKTCLNSADI  
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTDRIGAVQYTYEQRLFEFGFDKYSSKPD  
LNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRI PAMAAHLKG  
VITYAIGVAWAAQEELEVIATHPARDHSFFVDEFNLHQYVPRIIQNICTEFNSQPRN

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**FIGURE 114**

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTA  
TGCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT  
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCCACTACAGTTTTTCTCTGACTCTAAT  
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG  
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGAAACAAACATT  
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA  
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCCGAAAACCTCC  
 TCCCAGCCTTTTCAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTG  
 AACCCAGGAGAGACCCCTGTCACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC  
 CACCCTGAGCAGCCTCACTGGTGACCCGGTGTTTGAAGATGTGGCCAGAGTGGCTTTGATGC  
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC  
 AAGTGGGTGGCCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT  
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG  
 CCATCCGGAACCTACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAGATGTACAAGGGGACT  
 GTGTCCATGCCAGTCTTCCAGTCCTTGGAGGCCTACTGGCCTGGTCTTCAGAGCCTCATTGG  
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG  
 GGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA  
 CTTCCGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCT  
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGC GGAT  
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCCTG  
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG  
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGGTACA  
 TCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG  
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC  
 GAAATTTTCAGAAAAACACTGTTAGTTCGGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC  
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCA  
 CTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTT  
 AGACTCCTCATTAACCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA  
 AATTGCTTTTGGCTATCATAAAA

**FIGURE 115**

MPFRLLIPLGLLCALLPQH HGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE  
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL  
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM  
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK  
AIRNYTRFDDWYLVWQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYYTVWKQFG  
GLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRATGDPTLLELGRDAVESIEKISKVECG  
FATIKDLRDHKLDNRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY  
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGT  
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

**FIGURE 116**

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACA  
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
**AATG**CAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCCCTCAGAACCTC  
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA  
 AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
 GGATCCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC  
 ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG  
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA  
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
 GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT  
 GGTGCTGCCACTGTTTCGTCTGGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCCGTGG  
 TGGTCTCCAGACACCTTGAAAATAACCAATTACCCCCAGAAGTTAATCAGCTGCAGAAGG  
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT  
 CTCAT**TAG**GTTTGCAGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC  
 ATGAGGGGACAAGTTGTGTTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
 TGAAGGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
 CTGGGAAAAGTGACTTCATCCCTTCGGTCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
 TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA  
 TACACCCAGCACTTGCAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTGAG  
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
 GGCTTGGAGAGCCCACTTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
 TGTTGAGTTCACCTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
 AGGTGACCTGGAGGAAGGTCACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
 CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTTC  
 TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
 AAAAAAAAAA



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## **FIGURE 117**

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLWMWSPVIAPGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTS  
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILILV  
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation sites.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins homology.**

amino acids 92-119

#### **Integrins alpha chain protein homology.**

amino acids 232-262

0304193-0304193

**FIGURE 118**

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGGCGAACCCCTTGCGGCGCAAGGG  
GTTNGCGAACCCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC  
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

[illegible][illegible]

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**FIGURE 120**

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVNVVASECGFTDQ  
HYRALQQLQRDLGPHHFNVLAFCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG  
AHPAFKYLAQTSGKEPTWNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

FIGURE 120

**FIGURE 121**

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGCC**ATG**GCTGTCTACGTCGGGATGC  
 TGGCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGGCCCGGGCCGCCCTCTCT  
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCCTCAGTTCCAGAGAGGTGGATCG  
 CATGGTCTCCACGCCCATCGGAGGCCTCAGCTACGTTCAAGGGGTGCACCAAAAAGCATCTTA  
 ACAGCAAGACTGTGGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC  
 TTGGTCGTCTCCATGAAGACGTACGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA  
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC  
 CTAACCTCCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTTCTGGTG  
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCTCAAGAAGGTGGGCTGCAA  
 GGCCCTTGTGTTCCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCTGAAGCAGATCT  
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCTTGAAGAGTCAGAGGCTCCCAGATCTGACC  
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGGACCTGCTCCTGGATGAAGTGGTGGCGGC  
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACCAGCAGTTCTGTCTGCCATG  
 ACCCATCAACATCCAGTTACCTCGGGGACAACAGGCAGCCCCAAGGGGGGCCACCCTCTCC  
 CACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC  
 ACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCGTGGCAG  
 GCACAATGATGTGTCTGATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGC  
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGAT  
 GTTCGTGGACATTCTGAACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG  
 GTGTCAATTGCTGGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT  
 ATGAAGGACCTGGTGGTTGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTT  
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGG  
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGC  
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT  
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTCGCCACAATGAATGAGCAGGGCTTCTGCA  
 AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGGTGGTGAGAACATCTACCCCGCAGAG  
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA  
 CGATCGGATGGGGGAAGAGATTTGTGCCTGCATTGCGCTGAAGGACGGGGAGGAGACCACGG  
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC  
 GTGTTTGTACAAACTACCCCTCACCATTTCAAGAAAGATCCAGAAATTCAAACCTTCGAGA  
 GCAGATGGAACGACATCTAAATCTG**TGA**ATAAAGCAGCAGGCCTGTCTGGCCGGTTGGCTT  
 GACTCTCTCCTGTCAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCAGCACCCAGTTC  
 TGAGCCAGGCACATCAAATGTCAAGGAATTGACTGAACGAACCTAAGAGCTCCTGGATGGGTC  
 CGGGAACCTCGCCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG  
 TCCATCCCCACATTCCCCTGTCTGTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT  
 GAAAAAAAAAAAAAAAAA

**FIGURE 122**

MAVYVGMLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ  
GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG  
DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVF PKQFKTQQY  
YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLP GTLLLDEVVAAGSTRQHLDQLQYN  
QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY  
HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY  
DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTF AHFPEDTVEQKAESVG  
RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGD VAT  
MNEQGFCCKIVGRSKDMIIRGGENIYPAELEDDFFHTHPKVQEVQVVGVKDDRMGEEICACIRL  
KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domains:**

amino acids 140-161, 213-229, 312-334

**Putative AMP-binding Domain Signature:**

amino acids 260-271

**N-myristoylation Sites:**

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,  
314-319, 318-323, 379-384, 380-385, 409-413

**N-glycosylation Site:**

amino acids 282-285

**FIGURE 123**

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA  
TGATCCTGCCCCAACCCCTGTACCATTCGCTGGGTTC CGTGGCAGGCACAATGATGTGTCTG  
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC  
CATCAGCAGAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTTCGTGGACATTCTGA  
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC  
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT  
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCCTGAGGACACTGTGG  
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG  
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT  
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT  
ATTGGACAGGAGATGTCGCCAC

**FIGURE 124**

GAGCAGGACGGAGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC  
AGGCTGGCTGCTGCTGCTGCTGCTTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG  
TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC  
GTGGACGTCTGCACCGAGGCCGTGGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC  
AGTGCGGGGTTCGGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC  
TTCTGGCGTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC  
ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCCGCCCAACGGCGTGGAGTG  
CTACAGCTGTGTGGGCCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCGTGAGCT  
GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACCTTGACGGCA  
GCTAATGTGACTGTGTCCTTGCCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA  
TGGAGTAACAGGCCCAGGGTTCACGCTCAGTGGCTCCTGTTGCCAGGGGTCCCGCTGTAAC  
CTGACCTCCGCAACAAGACCTACTTCTCCCCTCGAATCCCACCCCTTGTCCGGCTGCCCCCT  
CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG  
ACCCACATCCACCACCAAACCCATGCCAGCGCCAACCAGTCAGACTCCGAGACAGGGAGTAG  
AACACGAGGCCTCCCGGGATGAGGAGCCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC  
CGCAGCAATTACAGGGCAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAAGGCTG  
TGTGGCTCCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTG**T**  
**GAG**GCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT  
CATCACTTCTGTTCCCACTGACTGGGCTGGCCCAGCCCCTGTTTTTCCAACATTCCC  
CAGTATCCCCAGCTTCTGCTGCGCTGGTTTTCGGCTTTGGGAAATAAAATACCGTTGTATAT  
ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC  
TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTCACGGGGAAGGTG  
AGAGAGAGGATGCTAAGCTTCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG  
GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCCTACTCCCCGCATCTTTGGG  
GAATCGGTTCCCCATATGTCTTCCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC  
CCAATTCGCCCTATAGTGAGTCGTA



**FIGURE 125**

MDPARKAGAQAMIWTAGWLLLLLLLRGGAQALECYSCVQKADDGCSPNKMKTVKCAPGVDVCT  
EAVGAVETIHGQFSLAVRGCGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNALNLTSRAL  
DPAGNESAYPPNGVECYSCVGLSREACQGTSPPVVSCYNASDHVYKGCFDGNVTLTAANVTV  
SLPVRGCVQDEFCTR DGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRI PPLVRLPPPEPTT  
VASTTSVTTSTSAPVRPTSTTKPMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSG  
QYPAKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL

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[illegible]

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**FIGURE 127**

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK  
CSFNQKPRAPGDEEAQVENLITANATEPQKQRTevQPSGGSLWNLRRLLLEPLDANVDA

094901 2567460

**FIGURE 128**

AAACTTGACGCC**ATG**AAGATCCCGGTCCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT  
CCTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG  
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT  
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAAGGAACTTCCTTT  
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAG**T**  
**G**ACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT  
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA

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**FIGURE 129**

MKIPVLPVAVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKDE  
FLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

TOEEO" aBbTHeO

**FIGURE 130**

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCC**ATG**GGGGGTGGAGATTGC  
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTC  
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC  
TTTGCCGGCCACTCA**TGA**GAGTGTTTTTGTGTAAAGTATTTTTTTAGAATACTGTTGACTTCT  
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA  
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT  
AGGTTCAAGGTTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATC  
TTCATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT  
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCACAAATGTGATTGTTAATTTAAA  
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT  
AAAAGTTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

[illegible]

**FIGURE 132**

GGGGAATCTGCAGTAGGTCTGCCGGCG**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG  
GCTGCTGTTGTTCCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA  
AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC  
TGCAGCTGCTACCATGGTGT CATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG  
GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA  
GACTGTACCGGGAAAATGACTGCATGTTCCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT  
TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCA  
GGTTCCTAAATGGATGGAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC  
ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT  
CCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTGAGCAGCACAGTG  
GCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG  
ATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTTGTTGATGCAGAATACACCAAAAAC  
CAGGCCTGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT  
GGATCACTGCAAATACAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA  
AACACCTCTTCCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATTCCTC  
TATCCACAGCTGAAGCCATGGGTTCCTATATCCCAGTCAAACAGATCTCTCCAATGTCCA  
AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA  
GCCAGTTTATTAGGAACCATTGTCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG  
AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT  
TCCCAAAATGTTGAAAACCTGAACTA**TAG**TAGTCATCATAGGACCATAGTCCTCTTTGTGGCA  
ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA  
TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA  
AAGATTTAAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA  
CCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCATTTTCTTAAGACCAATC  
ACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA  
TGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCATTTGGAAGTAGTACAA  
CTCATTGCTGGAATTGTGAAATTATTC AAGGCGTGATCTCTGTCACTTTATTTTAATGTAGG  
AAACCCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG  
TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTA AAACCATAACTCTGTTACTCAG  
GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT  
TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA



**FIGURE 133**

MEWWASSPLRLWLLLFLLLPSAQGRQKESGSKWKVFIDQINRSLENYEPCSSQNCSCYHGVIE  
EDLTPFRGGISRKMAEVVRRKLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIGRLPD  
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDL  
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD AEYTKNQAWKSMKDT  
LGKPAAKDVHLVDHCKYKYL FNFRGVAASFRFKHLFLCGSLVFHVGDEWLEFFYPQLKPWVH  
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY  
NVTRRKGYDQIIPKMLKTEL

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**FIGURE 134**

CACCCCTCCATTTCTCGCC**ATG**GGCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT  
 TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT  
 GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA  
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTTGTTGGGCAGC  
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCTTCAG  
 AGGTCACTGTATGTGGCCTGCACTGCCCTGGCCTTGCAGCTGGTGATGCGGTACTGGGAGCC  
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGGCCACCTGGGTGCCGC  
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT  
 GACTATGCTGAGCTCATGGGCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC  
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG  
 TGGAGCTGCTGACAGTGCTGTGGGTGGTGCCTACCCTGGGCACGGACCGTCTCCTCCTTGCT  
 TTCCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT  
 CCGGGCCCAGCTACAAAGAAAACCTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**  
**G**AGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCCTCTCCCACTGAATTCTAAATCCTTAAC  
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT  
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCTAAATTCTGAGTTTCAGCCA  
 CTGAACTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC  
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC  
 CTGACCACTCCCCCTGGCACTGTTACTTGCCTCTGCGCCTCAGGGGTCCCCCTTCTGCACCGCT  
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA  
 GGCCCCAACCTTGCCTCACCCTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT  
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACTCGATGACTTGGGGCTC  
 CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAAGTCAGCCTTTTTCTAAAAAAA



**FIGURE 136**

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA  
 AGAAATTGCCAAACCATGTCTTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT  
 TTTAATTAAGCATGGAATACAGAAAACAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT  
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA  
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG  
 AGCTGCTGTGG**ATG**GCCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCAGTACTGAGATCC  
 CTCAAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT  
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT  
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT  
 CTGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC  
 TTGGGGTGAAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTAGGCCAAG  
 AGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCCTTAGAGGATGAACACCTTCTTTATGGT  
 GACATAATCCGACAAGATTTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGC  
 ATTCAGGTGGGTAACTGAGTTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG  
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT  
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAACCCATAT  
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAA  
 TGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTCACGTAAAACCCATCAAGTTT  
 GAAGATGTTTATGTCGGGATCTGTTTGAATTTATTAAAAGTGAACATTCATATTCCAGAAGA  
 CACAAATCTTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG  
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTTGGCAGGTCATGCTAAGGAACACC  
 ACATGCCATTAT**TAA**CTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA  
 GTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTTACACTG  
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTC  
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAAATATAAAGGAATTGGAGGTTTTTGCTAAA  
 GAAATTAATAGGACCAAACAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGG  
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAAACAATGTAGAGTTTTATTTATTG  
 AACAAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA  
 TGTTAGTTCTGTGTCAAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT  
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAAATTA  
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT  
 CATTCTTTACATGCAAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC  
 TCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGGACTTTGTAAAT  
 ATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

**FIGURE 137**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD  
FHFTLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EK  
EDKMLALSLEDEHLLYGDIIRQDFLDYNNLTTLKTIMAFRWVTEFCPNAKYVMKTD TDVFIN  
TG NLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSGLGYIMSRD  
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG  
FSSKEIITFWQVMLRNTTCHY

T08280"266Th660

**FIGURE 138**

CCTCTGTCCACTGCTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT  
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA  
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA  
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC  
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT  
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC  
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA  
AAAAACATTGCAAACATGTGTCGTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC  
AAGCCTGTTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT  
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT  
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT  
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

**FIGURE 139**

MKFTIVFAGLLGVFLAPALANYNINVNDDNNNAGSGQQSVSVNNEHNVANVDNNGWDSWNS  
 IWDYGNNGFAATRLFQKKTCTIVHKMNKEVMPSTQSLDALVKEKKLQKGPGGPPPKGLMYSVN  
 PNKVDLLSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

**FIGURE 140**

CATTCTGAACTAATCGTGTCAGAATTGACTTTGAAAAGCATTGCTTTTTTACAGAAGTATA  
 TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCG  
 CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTCCTATTGCTTACTGATTTTTT  
 TGAGTTAAGAGTTGTTATATGCTAGAAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA  
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTTTACATG  
 CAAGCTTATAGTTGAAATATTTTTTCAGGAATTAC**ATGA**ATGACAGTCTTCGAACCAATGTGT  
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT  
 CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAAT  
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAAGCCAACTATGAATTAC  
 TGGAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTAAAAGCAAAGGGA  
 TTGAATCCGGATGGAACCTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC  
 ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG  
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAGAAAA  
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG  
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA  
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT  
 GGTCTCTCTCACCTTAAGGCCAAGCATAACCAGAGATGATTTAAAAGTTCAAACAGACATGG  
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG  
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT  
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG  
**CTGA**CTTTCTCTTCCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT  
 ATGGACTCAATCAAAAACATTAAACGCAAACTGATTAGGATTTGATTTCTTGAAACCCTCTA  
 GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTTGCACATT  
 AAAATGCCCTAGCAGTATCTAATTAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT  
 TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTT  
 ATACAGATAAAATTGCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT  
 ACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAAATACAAAT  
 CTTGTTTTTTCTAAAAAAAAAAAAAAAAAAGT



**FIGURE 141**

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRLY  
TRKKPNYELLEKEVEKRRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK  
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSRTRSRSRSHTPRRHYN  
NRRSRSGTYSSRSRSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRRSQ  
SKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKS KHHGGSRS GHGRHR

09499.08280  
T08280"266F4660

**FIGURE 142**

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA  
TTTTTTGAANNTATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTTACAGAAATATAT  
TANCTTTTTAGAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT  
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNNTATTGCTTACTGATTTTTTTTG  
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAAGA  
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTTTGTTTACATGCA  
AGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT  
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA  
GATTCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTTTGGTACTACAGAAGAGGAAATCC  
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAAGCCAACTATGAATTACTG  
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTTAAAGCAAAGGGATT  
GAATCCGGATGGAAGTCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

**FIGURE 143**

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGT**CATGGC**  
 GGTCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCACCCTCATGCACAGGCTGGCGC  
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGGATACAAGCACCCG  
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG  
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCCGAGATGCCCCGTTCAGCTGG  
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGCTTCTTCCTGGAGTACCAGTGG  
 TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTCACAGAGGCCTACTACTACAT  
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT  
 CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC  
 TCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGCCATGCTGGTGCAAGTGGTGCG  
 GGAGGAGACCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACTTAGAGC  
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCCTGTGGCCAAGCTGGCTATCCGCGTG  
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCCTCACCTTCCCAGGCCTGCGGCTGGC  
 CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCCTCCTGC  
 ACACCAGCTTCCTGTCTCCCCTGTTTCATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC  
 TTCCTGCACCAGCCGCCGTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA  
 CTCTGGGCGCCTCTGGTTGCTGGTGGTGTCTGTGCCTGCTGCGGCTGGCGGTGACCCGGCCCC  
 ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC  
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT  
 GAGCTTGACGTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC  
 TGGGAGGCTATTCTGGGGCCTGGGCCCAGCTCCTCTACTATCCCCGACCCATCCTCAGCC  
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG  
 GGCCCTGGGTGGCCTGCTTACTCCCCTCTTCCTCCGTGGCGTCTGACCTACCTCATCTGGT  
 GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA  
 GGCTCC**TAG**CTGCCTGCAGACCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA  
 CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC  
 GCGTTCCCTTCACCACAGTGCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA  
 GAACTGTCTCTCCTGGGCCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG  
 TGCCAGGTTTGTAGTGGCGAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAAGGAGCATGCC  
 GATTTTAA

**FIGURE 144**

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE  
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY  
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGGERSVCLTFAFLFLLLAMLVQV  
VREETLELGLEPGLASMTQNLLEPLLKKQGWDWALPVAKLAIRVGLAVVGSVLGAFLTFFPGLR  
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA  
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT  
VVS LQYLTPLILT LNCTLLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAA RI  
AGALGGLLTPLFLRGVLAYLIWWTAA CQLLASLFGLYFHQHLAGS

**FIGURE 145**

CGTTNGCACGCGTCAATGGCGGTCCCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCAC  
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT  
TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC  
CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC  
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC  
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT  
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT  
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTTCCTGACAGTGACACGGCTGTACTTCAGC  
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC  
CATGCTGGTGCAAGCG

**FIGURE 146**

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTT  
AATCTGAAGGTTCTCAGTCAAATTCCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGC  
TTGGCTGGTTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGA**ATGA**AGG  
CGCTTCTGTTGCTGGTCTTGCCCTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACCTTCTTG  
TATTCAGAACTCTGTAAAGGTGCCTCCCCTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTG  
TCCAGACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA  
TGACAGACGAGCCTGGCCTAGACAACCTGCCTACGTGTCCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCA  
GTGGACTCTGGCCGGAGCAACCGAAGTGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA  
AAAAATAAATCGAGCTTTGAGTGTTCTTGAAGGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCGACCAGG  
GCAGGGAAAATTCGAAAACACCACTGCCCCCTGAAGTCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAA  
ATTACCAGCATCAAGATCAATCGAGTAGATCCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC  
CCCCTGGTCCATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAG  
GAGACATCATTTCTAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCCTGCGG  
CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGCAGCAGGAACAATGGACAGGCCCC  
GGATGCCCTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA  
TAAACTGGTGCGCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA  
CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAGAAAG  
TGCGGCTCATCTGATTACAGGCCAGTGAAAGACGTGTTACCTCGTCGTGTCCCGCCAGGTTCCGGCAGCGGAGCC  
CTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT  
CCCAAGCCCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCT  
CGGCATGACCGTCGCAGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTGTCATCAGTTGAGCCCCG  
GAGGAGTCATAAGCAGAGATGGAAGAATAAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACCTGACA  
GAGGTGAGCCGGAGTGAGGCAGTGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGT  
CAAAGAGTATGAGCCCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCA  
GTGACTGGTCCCCATCCTGGGTGATGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTA  
CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTT  
TTTCATCAAATCCATTGTTGAAGGAACACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTG  
CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA  
ATTACTCTAACTATTGTTTCTTGGCCTGGCACTTTTTTA**TAGA**ATCAATGATGGGTGAGAGGAAAAACAGAAAAA  
TCACAAATAGGCTAAGAAGTTGAAACACTATATTTATCTTGTGAGTTTTTATATTTAAAGAAAGAAATACATTGT  
AAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATATGATTCCAAAAAAATTA  
AACTACTAGTTTTTTTTTTCAGTGTGGAGGATTTCTCATTACTCTACAACATTGTTTATATTTTTTCTATTCAAT  
AAAAAGCCCTAAACAACATAAATGATTGATTTGTATACCCCACTGAATTCAAGCTGATTTAAATTTAAATTT  
GGTATATGCTGAAGTCTGCCAAGGGTACATTATGGCCATTTTTTAATTTACAGCTAAAATATTTTTTAAATGCA  
TTGCTGAGAAACGTTGCTTTTCATCAAACAAGAATAAATATTTTTTCAGAAGTTAA

**FIGURE 147**

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDGCASLTAT  
APSPEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRS  
FKKINRALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDP  
SESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLL  
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVRKVDEPGV  
FIFNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRVQRS  
PDIFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHRE  
WDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV  
KEYEPQEDCSSPAALDSNHNMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV  
GGYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI  
TLTIVSWPGTFL

**FIGURE 148**

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT  
GCACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAA**ATG**GTGCTGACCATCT  
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC  
AATGTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC  
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC  
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT  
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG  
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAC  
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT  
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG  
TGCAGACATTCATGTT**TAG**GATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC  
TTGGTTTACACTCAAAAGTCAAATTAAATTCTTTCCCAATGCCCCAACTAATTTTGAGATTC  
AGTCAGAAAATATAAATGCTGTATTTATA



Figure 1 is a schematic representation of the experimental design. It shows a sequence of five steps: 1. Pre-test (N=10), 2. Training (N=10), 3. Test (N=10), 4. Post-test (N=10), and 5. Follow-up (N=10). Each step is represented by a box containing a number and a description. Arrows indicate the flow from Pre-test to Training, Training to Test, Test to Post-test, and Post-test to Follow-up. A feedback loop arrow points from the Post-test box back to the Training box.

Figure 1 is a schematic representation of the experimental design. It shows a sequence of five steps: 1. Pre-test (N=10), 2. Training (N=10), 3. Test (N=10), 4. Post-test (N=10), and 5. Follow-up (N=10). Each step is represented by a box containing a number and a description. Arrows indicate the flow from Pre-test to Training, Training to Test, Test to Post-test, and Post-test to Follow-up. A feedback loop arrow points from the Post-test box back to the Training box.

[illegible]

**Figure 6**

Panel A shows a bar chart of the number of cases by age group (0-4, 5-9, 10-14, 15-19, 20-24, 25-29, 30-34, 35-39, 40-44, 45-49, 50-54, 55-59, 60-64, 65-69, 70-74, 75-79, 80-84, 85-89, 90-94, 95-99) and sex (Male, Female). The y-axis ranges from 0 to 100. Panel B shows a bar chart of the number of cases by age group (0-4, 5-9, 10-14, 15-19, 20-24, 25-29, 30-34, 35-39, 40-44, 45-49, 50-54, 55-59, 60-64, 65-69, 70-74, 75-79, 80-84, 85-89, 90-94, 95-99) and sex (Male, Female). The y-axis ranges from 0 to 100.

**FIGURE 151**

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVPKGRWVLITCCAPQPPPPITYSL  
CGTKNIKVAKKVVKTHEPASFNLNVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK  
PVSELRANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCHRQPANFSFLP  
SQTSDWFWCQAANNANVQHSALTVVPPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG  
GFRIGNGEVRGRKAAAM

**Signal Peptide:**

amino acids 1-18

**N-glycosylation Sites:**

amino acids 86-89, 132-135, 181-184

**FIGURE 152**

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG  
CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGT  
CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA  
CTTTTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAAA  
CTAAATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACT  
TACAGAGCAACTGCGTGACATTGAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGC  
AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT  
TTCGATGGGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC  
TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCCTCCATT  
ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC  
CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCAC  
AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCA  
TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACG  
GTCTTGATCAAACTCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGT  
GGCCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCCTT  
TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC  
TGATGGAATTCCTGCACTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTTCTTTCTTC  
TCTTTTTGTTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT  
GTCAGTAAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG  
AATTTTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTAT  
TGTTCTGTACTGATATTTAATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 153**

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFEL  
HYDCGNKTVTPVSPPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR  
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS  
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 224-246

**N-glycosylation site.**

amino acids 68-72, 82-86

**N-myristoylation site.**

amino acids 200-206, 210-216

**Amidation site.**

amino acids 77-81

**FIGURE 154**

GGGAAAGCCATTTTCGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG  
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAATGGAG  
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG  
GTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAATCATGAACTCTGGCTGTTGATCAAAA  
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAGAAGCTAGCAGAAGAC  
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT  
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAAC  
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC  
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT  
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAAACCTTGCAGCAAGGGACC  
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTTCTGTAT  
CATCCTTTTCAATAAACTGTATTCATTTTGAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 155**

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA  
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGGQPTEQHFWARL

20220225T1550

**FIGURE 156**

GTTCTCTCTTCCGAGGCAAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**  
 CTCTTGTGGCAGGTAACCTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTTCGTCTA  
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCCTCAGCCGGGCCCC  
 AGAACTGCCCCCTCCGTTTTGCTCGTGCAGTAACCAGTTCAGCAAGGTGGTGTGCACGCGCCGG  
 GGCCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA  
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTTGCAGT  
 TGGGCAGGAACTCCATCCGGCAGATTGAGGTGGGGGCCTTCAACGGCCTGGCCAGCCTCAAC  
 ACCCTGGAGCTGTTTCGACAACTGGCTGACAGTCATCCCTAGCGGGGCCTTTGAATACCTGTC  
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCCATCGAAAGCATCCCCTCTTACGCCTTCA  
 ACCGGGTGCCCTCCCTCATGCGCCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT  
 GAGGGAGCTTTTTGAGGGGCTGTTCAACCTCAAGTATCTGAACTTGGGCATGTGCAACATTAA  
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAGGGAACCACT  
 TCCCTGAGATCAGGCCTGGCTCCTTCCATGGCCTGAGCTCCCTCAAGAAGCTCTGGGTCTAG  
 AACTCACAGGTCAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC  
 CAACTTGGCCCAACAATAACCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC  
 TGGTGGAGTTGCATCTACACCACAACCCCTTGGAACTGTGATTGTGACATTCTGTGGCTAGCC  
 TGGTGGCTTCGAGAGTATATACCCACCAATTCACCTGCTGTGGCCGCTGTCTATGCTCCCAT  
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCTCCTTCCAGTGCTCTGCCCCCT  
 TCATCATGGACGCACCTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT  
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC  
 CTCCCGCCACCCAAGGATCTCTGTCCTCAACGACGGCACCTTGAACCTTTTCCCACGTGCTGC  
 TTTTCAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG  
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAAACACCTCCAACCTACAGCTTCTTACCACAGT  
 AACAGTGGAGACCACGGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCTTA  
 CCACGTCCACTGGTTACCAGCCGGCATATACCACCTCTACCACGGTGCTCATTGAGACTACC  
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCCT  
 GGATGAAGTCATGAAGACCACCAAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGCTAG  
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACCAGCAGCGGAGTACAGTC  
 ACAGCCGCCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGC  
 AGCAGCAACAGCAGCTCCGTCCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCACAATTC  
 ATGACCATATTAACCTACAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGC  
 CTGGGGAACTCTCTGCACCCCCACAGTCACCACTATCTCTGAACCTTATATAATTCAGACCCA  
 TACCAAGGACAAGGTACAGGAACTCAAATAT**TGA**CTCCCCTCCCCCAAAAACCTTATAAAAT  
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTTTCTTGTA  
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAAAATTTAAAGA  
 CAAAAAGTCAAAACA



**FIGURE 157**

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAAASAGPQNCPSVCSCSNQFSKVVCT  
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS  
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY  
ISEGAFEGLEFNLYLNLMCNKIDMPNLTPLVGLEELEMMSGNHFPFIRPGSFHGLSSLKKLW  
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLP HDLFTPLRYLVELHLHNPWNCD CDILW  
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL  
KCRTPPMSSVKWLLPNGTVLSHASRHPRI SVLNDGTLNFSHVLLSDTG VYT CMVTNVAGNSN  
ASAYLNVSTAELNTSNYSFFTTVTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ  
TTRVPKQVAVPATD TTDKMQTSLDEVMKTTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRS  
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE  
NSLGNSLHPTVTTISEPYIIQTHTKDKVQETQI

**FIGURE 158**

CGCTCGGGCACCAGCCGCGGCAAGG**ATG**GAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCC  
TTCTCATCTCGTCTTGGCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAAATATCATG  
TGTGGGAGTGTGTGAATATGATCAGATTGAGTGGTCTGCCCCGAAAGAGGGAAGTCGTGGGTTATACCAT  
CCCTTGCTGCAGGAATGAGGAGAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTTTGAAACT  
GCAAGAGCTGCCGAAATGGCTCATGGGGGGGTACCTTGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAG  
TGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTT  
GTTGAAAGCTATCCCTAAATGCTCACTGTGAATGGACCATTATGCTAAACCTGGGTTTGTATCCAACTAA  
GATTTGTATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTCGTGATGGAGACAAC  
CGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACT  
CCACGTCTCTTCCACTCCGATGGCTCCAAGAATTTTGACGTTTTCCATGCCATTTATGAGGAGATCACAGCAT  
GTCCTCATCCCCCTTGTTCATGACGGCAGTGCCTTGAACAAGGCTGGATCTTACAAGTGTGCCTGCTTG  
GCAGGCTATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAACTGCTCAGACCCTGGGGGCCAGTCAA  
TGGGTACCAGAAAATAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAAAATTGGCACCGTGGTGTCTT  
TCTTTGTAACTCCTATGTTCTTAGTGGAATGAGAAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGG  
AAACAGCCCATCTGCATAAAAGCCTGCCGAGAACCAAGATTTAGACCTGGTGAGAAGGAGAGTTCTCCGAT  
GCAGGTTCACTCAAGGGAGACACCATTAACACAGCTATACTCAGCGGCTTCAGCAAGCAGAACTGCAGAGTG  
CCCCTACCAAGAAGCCAGCCCTTCCCTTTGGAGATCTGCCCATGGGATACCAACATCTGCATACCCAGCTCCAG  
TATGAGTGCATCTCACCTTCTACCGCCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAG  
TGGGCGGGCACCATCTGCATCCCTATCTGCGGGAAATTTGAGAACATCACTGCTCCAAAGACCCAAGGGTTGC  
GCTGGCCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGGTGCATGACGGCAGCCTACACAAGGGAGCGTGG  
TTCCTAGTCTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACTGTGTACTGACCTGGG  
GAAGGTCACCATGATCAAGACAGCAGACCTGAAAGTTGTTTTGGGGAAATTTACCGGGATGATGACCGGGATG  
AGAAGACCATCCAGAGCCTACAGATTTCTGCTATCATTTCTGCATCCCACTATGACCCCATCTGCTTGATGCT  
GACATCGCCATCCTGAAGCTCCTAGACAAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCTCGCTGCCAG  
TCGGGATCTCAGCACTTCTTCCAGGAGTCCACATCACTGTGGCTGGCTGGAATGCTCTGGCAGACGTGAGGA  
GCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAG  
CATGAGGACCATGGCATCCCACTGAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCTTC  
TGATATCTGCAGTGCAGAGACAGGAGGCATCGCGGCTGTGTCCTTCCCGGGACGAGCATCTCCTGAGCCACGCT  
GGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCCACTGCCTTACCAAG  
GTGCTGCCTTTTAAAGACTGGATTGAAAGAAATATGAA**TGA**ACCATGCTCATGCACTCCTTGAGAAGTGTTTC  
TGTATATCCGTCTGTACGTGTGTCAATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTTGGCCTGTGAACTTGG  
CTGTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAGTAGACCTCCATTGCTGGTAGGCTGAT  
GCCGCGTCCACTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAAGAAGACC  
ATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCCAACTTTCAGTTATACGAATGCCATCAGCTTG  
ACCAGGGAAGATCTGGGCTTCATGAGGCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCC  
CAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTTTGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCC  
CCATCTCTTGTACACATTTTAATAAAATAAGGGTTGGCTTCTGAACACAAAAAAAAAAAAAAAAAAAAAAAAA  
AAA  
AAA

**FIGURE 159**

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV  
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGD  
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD  
GDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFGHAIYEEITACSSSPCFHDG  
TCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV  
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLH  
QLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK  
WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE  
RTVVVAAHCVTDLGKVTMIKTADLKVVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLD  
ADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVVLADVRSPGFKNDTLRSG  
VVSVDSSLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR  
WHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

**FIGURE 160**

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTTCGCAATCAGATTGGAAAAAGCTCAACTTGA  
AGCTTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAAC**ATG**GGC  
TTCAACCTGACTTTCCACCTTTCCTACAAATTCCGATTACTGTTGCTGTTGACTTTGTGCCT  
GACAGTGGTTGGGTGGGCCACCAGTAACACTTTCGTGGGTGCCATTCAAGAGATTCCTAAAG  
CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAACTCTGACT  
AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACCTGTCCTTCTGTGTCTCCTTACCTCAG  
AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC  
CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTGCCTATC  
CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT  
CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT  
TTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC  
TGCTTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA  
GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG  
GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT  
AACAACTACTGGGGATGGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAG  
AATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAG  
ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGG  
AGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA  
TATCAACATCACAGTGGATTTCTGGTTTGGTGCA**TGAC**CCCTGGATCTTTTGGTGATGTTTGG  
AAGAACTGATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA  
AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCTTTTTGTATTTTCTTAGCAGAGCT  
CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAGTCATTTTGATCATG  
AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT  
AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT  
TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCT  
CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTCAATTTATCCTGTACAATCATCT  
GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA  
GGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG  
CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCCAGGTATGCCT  
TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTTAAAGAGTTTTTGTAAAATGA  
TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATAAATA  
TGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

## **FIGURE 161**

MGFNLT FHLSYKFRL LLLLTLC LTVVGWATSNYFVGAIQEIPKAKEFMANFHKT LILGKGKT  
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV  
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKGKFNRAKLLNVGYLEALKEEN  
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGVTALSREQFFKVNG  
FSNNYWG WGGEDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR  
VWR TDGLSSCSYKLVSVEHNPLYINITVDFWFGA

### **Important features:**

#### **Signal peptide:**

amino acids 1-27

#### **N-glycosylation sites:**

amino acids 4-7, 220-223 and 335-338

#### **Xylose isomerase proteins:**

amino acids 191-201

**FIGURE 162**

CGTGGGCCGGGGTTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGCAAGTTCTC  
GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGGCCCCGCA**ATG**  
GCCCAGGCAGTGTGGTCGCGCCTCGGCCGCATCCTCTGGCTTGCCTGCCTCCTGCCCTGGGC  
CCCGGCAGGGGTGGCCGCAGGCCTGTATGAACTCAATCTCACCACCGATAGCCCTGCCACCA  
CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG  
CCCCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGGCTTACTGGCAA  
GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTTCGGCCACGTGCCCGGGGAATTCCCGG  
TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG  
GTCCTCCCCATCACAGAGTTCCCTCGTGGGGGACCTTGTTGTACCCAGAACAACCTTCCCTACC  
CTGGCCCAGCTCCTATCTCACTAAGACCGTCTCTGAAAGTCTCCTTCCCTCCACGACCCGA  
GCAACTTCCTCAAGACCGCCTTGTTTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG  
GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCT  
CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA  
CCGGGGACTTCTCCGCTCGCTGAAGCTGCAGGAAACCCTTCGAGGCATCCAAGTGTTGGGG  
CCCACCCTAATTACAGACCTTCCAAAAGATGACCGTGACCTTGAACCTCCTGGGGAGCCCTCC  
TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCTCCCGCTGGAGGAAGGGGAGTGCCACC  
CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCCCTGGGGACTAC  
TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT  
GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA  
TGTTGGCCTTCATCATGTACATGACCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG  
AACCCGGAGCCACCCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCCTTTCTTGCT  
GGAGACTCCATCTGAGTACCTGGAATTTGTTCTGAGAACCACGGGCTGCTCCCGCCCCCTCT  
ATAAGTCTGTCAAACTTACACCGT**GTGAG**CACTCCCCCTCCCCACCCCATCTCAGTGTTAA  
CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTTCAAT  
TGCGTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTCAGCCACTGCCACAAGCC  
CCTCCCTCTCTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA  
TAAGCCCCACTCGGTTACCACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT  
TTGATGCTTGGGGTGTTCGTGTTGACTCCTAGGTGGGCCTGGCTGCCCACTGCCCATTCCT  
CTCATATTGGCACATCTGCTGTCCATTGGGGGTTCTCAGTTTCCCTCCCCAGACAGCCCTAC  
CTGTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGGTTGTAC  
ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACA  
CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTTCAAGATGATCAGCTCTGTA  
TCTGGTTAAGTCGGTTGCTGGGATGCACCCTGCACTAGAGCTGAAAGGAAATTTGACCTCCA  
AGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCAGTTCTTGC  
GCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT  
AATACTGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTG  
AACTTTCACTGAGGAAAAGGCCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGG  
TGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA  
GATCGAGACCACCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAAGTT  
AGCCGGGCGTGGTGGTGGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATG  
GTGCGAACCCGGGAGGCGGAGCTTGACGTGAGCCAGATGGCGCCACTGCACTCCAGCCTGA  
GTGACAGAGCGAGACTCTGTCTCCA

**FIGURE 163**

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA  
LPADAHLYRFHWIHTPLVLTKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGF  
VVLPITEFLVGDLVVTQNTSLPWSSYLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDGTQ  
MVTEDSVVYYNYSIIIGTFTVKLKVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL  
GPTLIQTFQKMTVTNLFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD  
YCFSIRAENIISKTHQYHKIQVWPSRIQPAVFAPCATLITVMLAFIMYMTLRNATQQKDMV  
ENPEPPSGVRCCCQMC CGPFLLET PSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

**FIGURE 164**

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACG**ATG**GCACTGAGCTCCCAGATCT  
GGGCCGCTTGCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA  
CAACAGACGGGACAACCTTGCAGAGCTGCAACCCCAGGACAGAGCTGGAGCCAGGGCCAGCTG  
GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCCATCTGCATTTTCTGCT  
GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACG**TAG**AACCTACCTGCCCTG  
CCCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGAATAAAA  
TGGCTGGTTCTTTTGTTTTCCAAA  
AAA



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**FIGURE 165**

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH  
FPICIFCCGCCHRSKCGMCCKT

FOR 254450

**FIGURE 166**

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC  
 CTGGATCTTCCACC**ATG**TTTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC  
 ATCTCCCTGACTGTCTCTTACCCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG  
 AGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA  
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCCCTACACCAAC  
 GGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTGCAAGTGG  
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCC  
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG  
 GAGTCCTGGAACCTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC  
 GGTCTGTGGGGGTTAGGAGTGCTGATTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC  
 TGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCCAAAT  
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCG  
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCT  
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC  
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTGAGAGAGCCATGGTGAAGGCCTG  
 CCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA  
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCCAGAAGGAACCTGCATC  
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCC  
 TGTTGCTATCAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGA  
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG  
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAAATCTGC  
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCTGAAGAGGGAGAAGG  
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCAC  
 AAGGACAGGAGCCGCTCC**TGA**GCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA  
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCCACTGCTGTGTCTTTCCAGACTCCAGGG  
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCGAGCCGCAGCGGGATCCCTGT  
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA  
 CGAGATGCCTTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAGTGAACCTCCCCA  
 CCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT  
 GGCGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCG  
 CTCTCCAGGAAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGC  
 CTTGGAGCTCTGCAGACATGATAGGAAGGAAACTGTCATCTGCAGGGGCTTTCAGCAAATG  
 AAGGGTTAGATTTTTATGCTGCTGCTGATGGGGTTACTAAAGGGAGGGGAAGAGGCCAGGTG  
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTTCGTACTCCAGGCTAACCCTGAACTCCCC  
 ATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG  
 GAATGGTGGTGATTCCCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGA  
 AGGACACATCACGTTCAAGTACAGGCCACAAAACGGGGCACGGCAGGCCTGAG  
 CTCAGAGCTGCTGCACTGGGCTTTGGATTTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA  
 TGA

**FIGURE 167**

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIIVPAIFGVSGIRKLYMKSLLKIFAWATLRME  
RGAKEKNHQLYKPYTNGIIAKDPTSLEEEIKEIRRGSSKALDNTPEFELSDIFYFCRKGME  
TIMDDEVTKRFSAEELSWNLLSRTNYNFQYISLRLTVLWGLGVLIRYCFLLPLRIALFTG  
ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRPNGGICVANH  
TSPIDVIIILASDGYIAMVGQVHGGMLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ  
DKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYL  
LRMMTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTF  
KEEQQKLYSKMIVGNHKDRSRS

**FIGURE 168**

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGGCCCTCA  
CGTCTCCTCCAGGG**ATG**GCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC  
ACCTGGCAGGCCCAGGCTGTTCCCACCATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGA  
CGATACCTATGTGGGTGTGTCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG  
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCCAGGAGACCTGGGAGGAC  
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT  
CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG  
GCTCCCGGGAGCTCTACATGAGGCACTTTCCTTCAAGGCCCTGCATTTCTACCTGATCCGG  
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTTCG  
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT  
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCCACAGATTTGGGGAGAAGAGGCGGGGCTGT  
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTG  
GAAGACTCTGCTCTTGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTTGGGCCCC**TGA**AAGTCCA  
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG  
CAGCCTTGAGAAGCAAGAACATGGTTCCGGACCCAGCCCTAGCAGCCTTCTCCCCAACAGG  
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT  
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTTGCAATGTGGAGACA  
TGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

**FIGURE 169**

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHH  
ALLRESWEAAQETWEDKRRGLTLPPGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSREL  
YMRHFPEKALHFYLIRALQLLRGSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS  
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKTLLLAPGEFQLSGVGP

004193 0330  
T08280"266T460

**FIGURE 170**

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCA  
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG  
GTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC  
TATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCA  
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG  
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT  
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG  
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG  
GAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC  
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT  
GCGTTGCCAGGAACCCTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT  
GAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCCT  
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG  
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAAACTCCTAACATATGCCCCCAT  
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAATCCTAAAGGAAGA  
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCACTCAC  
TGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGCAGTG  
CACTCCCCTAAGTCTCTGCTCA

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**FIGURE 171**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT  
IQPEGGTIIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV  
YEHLSPKPKVTMGLQSNKNGTCVTNLTCCEHGEEDVIYTWKALGQAANESHNGSILPISWRW  
GESDMTFICVARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLW  
FLKRERQEEYIEEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPANTVYSTVEIP  
KKMENPHSLLTMPDTPRLFAYENVI

094193.08301  
T03280.256T450

**FIGURE 172**

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC  
TCTGGACCCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGCTGACTTTCCCCCTGAAGTC  
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC  
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA  
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT  
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG  
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG  
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT  
GGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG  
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAACTTCTCAAGCCCC  
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCTCCATGGTCCTCCT  
GTGTCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC  
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGGAA  
ACTCCTAACATATGCCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA  
TAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAA  
AGATGGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAG  
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAAA



**FIGURE 173**

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT  
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA  
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA  
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGAGAGAA  
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG  
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT  
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA  
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA  
GGTTTGCACAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT  
GCCAATCGCTGCCTCCAGGCCCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTTGAGTGGAC  
ACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTATAAATTC  
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC  
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT  
TTTTCATGAAATTATTCCTCTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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**FIGURE 174**

MKMLLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ  
IHVLENSLVLKVHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLI  
NEKDGETFQLMGLYGREPDLSSEIKERFAQLCEEHGILRENIIDLSNANRCLQARE

103230" 26674660

**FIGURE 175**

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA  
TGGATTGAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG  
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC  
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG  
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA  
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC  
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA  
CATTCATCCAGAATCCTTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG  
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC  
TTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTATAGGTCTATTGCT  
TGTTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC  
TGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA  
TCAGTAGTTTGAAAAAAAAAAAA

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**FIGURE 176**

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA  
IPATTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNA  
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRL  
IHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

FORO" 2667460

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**FIGURE 177**

GTCGAATCCAAATCACTCATTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT  
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT  
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC  
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTG  
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTGAA  
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC  
CTGATCTTCACTAAAAATTGTAAAGGTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

read 268466

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**FIGURE 178**

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNQLQVAKLNPPPEALAAKLEV  
KHCTDQISFKKRLSLKKSWWK

T0230" 266T460

**FIGURE 179**

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG  
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG  
GAGCAGATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTC  
GAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG  
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG  
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG  
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCAC  
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA  
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC  
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTTCTTTATGAATTAAACTCG  
CCCCACCACCCCCTCA





**FIGURE 181**

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCCC  
TGGCTGGGCCTCAGACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC  
CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTGCCGCCGGCTCC  
AGTGTTTCCACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT  
ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGGCCACCTATTCCCAGGGCTTTACGGT  
ATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA  
CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG  
CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC  
GCCCCCTTCCATTTCAACATCCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACA  
TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG  
CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG  
TCAGGAGAGGCCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA  
GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGC  
TTCCACAGGGCCTGCCGCCTGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCG  
CACCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG  
ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT  
ATAAGAGCAGAGGCTGACACCTTCATGTTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC  
CTGGGTCTGTACAACCTTGCAGGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC  
AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCC  
TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCCG  
ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC  
TCATCGATATTATAGGGGTCCATCACAACCCAAGTGTGTGGCCGGATCCTGAGGTCTACGAC  
CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCTTTCTC  
CGCAGGGCCCAGGAAGTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCCTGG  
CGTTGATGCTGCTGCACTTCGGGTTCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAA  
TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCA  
**GTGA**CTTTCTGACCCATCCACCTGTTTTTTTTGCAGATTGTCATGAATAAAACGGTGCTGTCAA

**FIGURE 182**

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWG  
HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF  
IRFLKPWLGEIGILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS  
SRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY  
LSHDGRRFHRACRLVHDFTDVIRERRRTLPTQGIDDFKDKAKSKTLDFIDVLLLSKDEG  
KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCRQEVQELLKDRDPKEIEW  
DDLAQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW  
PDPEVYDPERFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT  
EPRRKLELIMRAEGGLWLRVEPLNVGLQ

**FIGURE 183**

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC  
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA  
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA  
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG  
AAAGCAGACTCAAGTACCAACATTTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT  
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA  
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT  
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAAC  
AGTGTGGAGAAAAACTAGGCAAACTACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT  
ATGTTTTGCACAAAAAAAAAAAAAAAAA

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**FIGURE 184**

MYKLASCCLLFTGFLNPLLSLPLLDSREISFQLSAPHEDARLTPEELERASLLQILPEMLGA  
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FOI2020-254450

**FIGURE 185**

GAACATTTT TAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT  
GGGGTTGCTGGTTTAAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA  
CCACCTCCGCCAGGAAGTGCAGGCCCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC  
AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT  
CCAGCTTCCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA  
GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGGAAGATGGAGGTCAAGCAGA  
AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT  
CAGGGGTT CAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG  
GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATCGCCCACAAGCCTTACTCACCTCTCTCT  
AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA  
CAAGCTCAGGAGGCGAATAAATGTTCAAAGTGT

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**FIGURE 186**

MPSPGTVCLLLLGMLWLDLAMAGSSFLSPEHQRVQQRKESKKPPAKLQPRALAGWLRPEDG  
GQAEGAEDELEVRFNAPFDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADKO

094900Z FEB 80 266THAD

**FIGURE 187**

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCCTCGTCCAGTACCTC  
GTGAACCCCGGGGTGCTCCGCACGGACCCAGATGTCAAGAATATGAACACGTGGCTGCTGT  
TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG  
CTCCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT  
GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAGAGCTGCTCATC  
TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT  
GTCCCCCGTGTGCGCATGTGTTCAAGGTGTCAGCCTCTCCAGAAAGTGAGATCATGGACAAAAA  
GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCCCAGCAAGAAGCTGAAC  
TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCA  
GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT  
CCAAAAACACAAGTAGAAATTTCTAACAAATGAAATATATTACAGGCAGGTACCCACTAACCA  
AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC  
AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT  
AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAGCG  
TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTCTGTGGAC  
ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA  
ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA  
GCATCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCACCAAGA  
GCCTCCTTGTTTCATAACCACAGGTTACCCTACAAACCACTGTCCCCACACAACCCTGGGGAT  
GTTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCCTGAGGGTTGA  
ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 188**

MNTWLLFLPLFPVQVQTLIVVIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLSPRSPQGW  
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ  
AQQEAELTPRPAGVVPGA

09493 0667660



**FIGURE 189**

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACC**ATG**GCCAAG  
ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT  
ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG  
TGCCCAAGCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG  
GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACTGGGAGACTGGGGATGA  
CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG  
AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAA  
GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTCACCCCACTCTCCGATTTGGAGGGAA  
GCGGTTGATGGAGAAGGCTTCCCTCCCCTCCCCTCCCCTTGGGGCTTTGTGGCAAAAATCCTA  
TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT  
ACTAACAGACTTGCTACTCACTGGGAACCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG  
CTGTTTCCTCTGTCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC  
TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGCTG  
GGCCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTCGGCTGTCACCACCTTCA  
ACACGTACACCAGGATGGTGCTGGAGTTCAAGTGCAAGCA**TAG**TAAGAGCTTCAAGGAAAAC  
CCGAAGTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC  
CGTGGGTCCCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG  
GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG  
AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGGTTTGGGGA  
GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG  
TCTCTTGAGCATGGTTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC  
CTAAGGGATTCCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTCACCCAC  
CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC  
TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

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**FIGURE 190**

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP  
VSLDGDNTNTSTQEYVQYNWETGDDRFSFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR  
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL  
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSCQLGSRRLTTTCLE  
LWLGLLHGLALLHLLHGVGCHHLQHVVHVDGAGVQVQA

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**FIGURE 191**

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAG~~ATG~~TGGTTACCCCTTGGTCTCCTG  
TCTTTATGTCTTTCTCCTCTTCCTATTCTGTCATCTCCCTCACTTAAGTCTCAGGCCTGTCA  
GCAGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG  
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT  
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG  
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCCTCCTCCCAA  
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG  
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT  
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCCTTCCCCCTGCCCCGCCGTAGATTAG  
GACATTCGCCCCCTGTGTGCCACCAAACCAGGACTTTCCCCCTTGGCTTGGCATCCCTGGCTCT  
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACT  
ATGGCGATGGCCATGATGTTACAATCCCACTTGCCTGAATAATCAAGTGGGAAGGGGAAGCA  
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAA  
GGGAAGCAACAGGAACCTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGC  
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA  
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATTCCAAACTCTTTATTACTTTGGG  
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG  
AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC  
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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**FIGURE 192**

MWLPLGLLSLCLSPLPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGSME  
HRNHLCFCDLYDRATSPPLKCSLL

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**FIGURE 193**

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCGTGGAGCCAGGAGCGACGTCA  
 CCGCC**ATG**GCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTGATGCTT  
 GGATGTGCCCTTCCAATATACAACAAATACTGGCCCCCTCTTTGTTCTATTTTTTTACATCCTTTCACCTATTCC  
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAACTTGCCATCTTTC  
 TTACAACGGGCATTGTCTGTCTCAGCTTTTGGACTCCCTATTGTATTGTCAGAGCACATCTGATTGAGTGGGGA  
 GCTTGTGCACTTGTCTCACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTTCTTGGTCTTTGGAAG  
 CAATGACGACTTCAGCTGGCAGCAGTGG**TGA**AAAGAAATTACTGAAGTATTGTCAAATGGACTTCCTGTCATTT  
 GTTGGCCATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTA  
 GGTGCTCCCTTCTCACTTTTATTGTAAAGCATACTATTTTCACAGAGACTTGCTGAAGGATTTAAAGGATTTTCT  
 CTTTTGGAAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTTTGTGGTGTCTGCTGAATTTAAATAT  
 TTATGTGTTTTTCCCTGTTAGGTTGATTTTTTTTGGGAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA  
 TTTGCATTGGTTAGGAATTCAGAATTCGCCCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATTTAT  
 TAGCCTCCATTATTACAAAAAATTATAAAAAATAAGTTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATG  
 CAGACATACAGACGGTTGGCATACTGTTATAGACTGTATACTCAGTGCAAATATAGCTGCATTTATACCTCAGAG  
 GGGCCAAGTGTTAATGCCCATGCCCTCCGTTAAGGGTGTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG  
 AAAATTATTTTATGGAATTGCTACAGAGGAGTGCTTTCTCAATTGTTAGAAGAATTTATGTTAAACTTTA  
 AGGTAAGGGTGTAACAAACATTTTTTGAGATAAGGTTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGT  
 GGGGAAGAAATGACATTGAAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAAATTTGTGATCTCCTATC  
 AACCTTTTCATGTTTTACCCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGC  
 ATCATATATGCCAGAAACCTTCCTCTGCTTCCTCCTTTTGAAGTATTGTTGGTATGTTGTATATATTACATAAAA  
 TAACTTTTCAAATATAGTTTAATAACACTTAGAAGTGTTTACTTACCTGGAAAAATAATTGCTATGCCGTACATT  
 CAGAGTGGCCCCCTCCCCTGCAAGGCCTTGCCATGATTAAACAAGTAACCTGTTAGTCTTACAGATAATTTCATGCA  
 TTAACAGTTTTAAGATTTAGACCATGGTAATAGTAGTTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAG  
 TATTTTTAAGACAAGTTTCCCTGTATACCTCTGAAGTGTGTTTGAATTTGAGTTCATCATGATAGATCTGCTGTTT  
 CCTTATAAAAGGCATTTGTTGTGTGAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT  
 ACCTGACCAAAAAATTCAGTAACAGGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTATCAGGA  
 CTTTTTTTCAGGAGTGGGTATATAAAACATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTTGTATG  
 TTTATTCAGTATACTTACATAAAAAATTATTTGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGT  
 TTTATGAAGTTTATTTCTCAAGAAAATGGGAATAAATTTGGGATTTGTTTCAAGCTTTTTTACTAAAGATGCCTAA  
 AGCCACAGGTTTTATTGCCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCG  
 GCGTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGGCTTGTGGTATTATAATGTTTCAAGAGGAA  
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTCTTGTGCTTGTGATCTACTGGACTTT  
 TTTTTTGCAGGAAGTGCATTCTCTGGTCTTCCCTATTTTCTGTTCTGGATGTGAGTGCAGTGCAGTGCAGTGCAGT  
 TTTTATCCACTTGGCCACAGACTTTTTCTAACAGCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCAT  
 GTGTCTTTGACCTTGATATACTAGCTTGACATAGTGCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT  
 TTTCCATAGAATATGCACTGATACAACATTACCATTCTTCTATGGAAAGAAAACTTTTGATGATGAAACAATAA  
 AGATTTTTAATATCTATTTTAAAAA

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**FIGURE 194**

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM  
SNACKELAIFLT TGIVVSAFGLPIVFARAH LIEWGACALVLTGNTVIFATILGFFLVFGSND  
DESWQQW

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[illegible]

**FIGURE 196**

MDFLLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH  
NLSGLLGLSLRYNSLSELRAGQFTGLMQLTWLYLDHNNHICSVQGDAFQKLRRVKELTLSSNQ  
ITQLPNTTFRPMPNLRSDLSYNKLQALAPDLFHGLRKLTTLHMRANAIQFVPVRIFQDCRS  
LKFLDIGYNQLKSLARNSFAGLFKLTEHLEHNDLVKVNFAHFPRILISLHSLCLRRNKVAIV  
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRLTYIEPRIILNSWKSLSIT  
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVYAFHLCEDGAEPTSG  
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGTFEPATVALPGGEHAENAVQIHKVVTGTMA  
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQMAAMSAQEYYVDYKPNH  
IEGALVIINEYGSCTCHQQPARECEV



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**FIGURE 197**

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCCGGGTCCCTGCTGTGGCTGCAGCTCTGC  
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA  
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGGCGCCGTTGAGTTCCTGGCGGACAAGATGG  
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA  
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG  
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT  
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC  
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG  
CCCCGTGCGTGTCGCGAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG  
CTGTTTTCTGGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGCCGGGCGCGC**TGA**GCGTG  
GGCCCCGAGGACTGCGCGGACCCGTGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG  
GATCTGCGCGGCCCTGCTCCAGCCCCT

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Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.45	0.50	0	1
Marital Status	0.60	0.49	0	1
Education	12.5	1.5	9	16
Income	15.2	8.5	5	35
Health Status	0.75	0.43	0	1
Stress Level	3.2	1.8	1	5
Life Satisfaction	4.1	1.2	2	6
Work-Life Balance	3.8	1.5	2	5
Family Support	4.5	1.0	3	5
Community Involvement	2.5	1.5	1	4
Personal Growth	3.5	1.2	2	4
Financial Stability	3.0	1.0	2	4
Relationship Quality	4.0	1.1	3	5
Overall Well-being	3.8	1.3	2	5

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.45	0.50	0	1
Marital Status	0.60	0.49	0	1
Education	12.5	1.5	9	16
Income	15.2	8.5	5	35
Health Status	0.75	0.43	0	1
Stress Level	3.2	1.8	1	5
Life Satisfaction	4.1	1.2	2	6
Work-Life Balance	3.8	1.5	2	5
Family Support	4.5	1.0	3	5
Community Involvement	2.5	1.5	1	4
Personal Growth	3.5	1.2	2	4
Financial Stability	3.0	1.0	2	4
Relationship Quality	4.0	1.1	3	5
Overall Well-being	3.8	1.3	2	5

**FIGURE 199**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTT  
TGAGCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTT  
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCA  
TTGACGTGGTACAGCCTTTCCTTCATAACCATTTGCAAGGGATGCTGTGAAGAAGTGTTTTGC  
CGTGTGTCTTGCATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAG  
CTGGTGGACAGTTTTGTAACTATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT  
TGCAGCAATGTGTTGCTTGTGATTTCGAACATTTGAGGGTTACTTTTGGAAGCAACAATACAT  
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTTCTGTATCTTGTGGAGTGGAA  
TCTTCCTCATGTACCTGTTTCCTCTCTGGATGTTGTCCCACTGAATTCCCATGAATACAAAC  
CTATTCAGCAACAGCAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 200**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYLSFIP  
FARDAVKKCFVCLA

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**FIGURE 201**

TTGAGCGCAGGTGAGCTCCTGCGCGTTCCGGGGGCGTTCCCTCCAGTCACCCTCCCGCCGTTACCCGCGGCGCGC  
 CCGAGGGAGTCTCCTCCAGACCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT  
 GGGAGAGAAAAATTAGGGGGAGAAAGGACAGAGAGAGCAACTACCATCCATAGCCAGATAGATTATCTTACACTG  
 AACTGATCAAGTACTTTGAAAATGACTTCGAAATTTATCTTGGTGCCTTCATACTTGCTGCACTGAGTCTTTC  
 AACCACCTTTTCTCTCCAAGTAGACCAGCAAAAGGTTCTACTAGTTTCTTTTGATGGATTCCGTGGGATTACT  
 TATATAAAGTTCCAACGCCCCATTTTCATTATATTATGAAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT  
 TTTATTACAAAAACCTACCCTAACCATTTACTTTGGTAACTGGCCTCTTTGCAGAGAATCATGGGATTGTTGC  
 AAATGATATGTTTGATCCTATTCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTCCAAGTTTT  
 GGGAAAGAGCGACACCAATATGGATCACAAACCAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCCGA  
 ACAGATGTAAAAATACATAAGCGCTTTCCTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG  
 AGTTGCCAAAATTTGTTGAATGGTTTACGTCAAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTG  
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCAATTCAGATATTGACAAGAAGTTA  
 GGATATCTCATACAAATGCTGAAAAAGGCAAAGTTGTGGAACACTCTGAACCTAATCATCACAGTGATCATGG  
 AATGACGCAGTGCTCTGAGGAAAGGTTAATAGAAGTTGACCAGTACCTGGATAAAGACCACTATACCTGATTG  
 ATCAATCTCCAGTAGCAGCCATCTTGCCAAAAGAAGGTAATTTGATGAAGTCTATGAAGCACTAACTCACGCT  
 CATCCTAATCTTACTGTTTACAAAAAGAGACGTTCCAGAAAGGTGGCATTACAAATACAACAGTCAATTTCA  
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTTTACAGAATAAGTCAGATGACTTTCTGTTAGGCAACC  
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTTAGCCCATGGTCCCTGCCTTCAGAAAGAATTC  
 TCAAAAGAAGCCATGAACCTCCACAGATTTGTACCCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA  
 CAATGGATCATTCTGGAATGTCCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA  
 CTATACTCCTCCCTGGTAGTGTAAACCAGCAGAATATGACCAAGAGGGGTATACCCCTATTTTCATAGGGGTC  
 TCTCTTGGCAGCATTATAGTGATTGTATTTTTTTGTAATTTTCATTAAAGCATTTAATTCACAGTCAAATACCTGC  
 CTTACAAGATATGCATGCTGAAATAGCTCAACCATTATTACAAGCCTAATGTTACTTTGAAGTGGATTTGCATA  
 TTGAAGTGGAGATTCCATAATTATGTCAGTGTTTAAAGGTTTCAAATTTCTGGGAAACCAGTTCCAAACATCTGC  
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACATACACACACACGGACCAAA  
 ATACTTACACCTGCAAAGGAATAAAGATGTGAGAGTATGTCTCCATTGTTCACTGTAGCATAGGGATAGATAAG  
 ATCCTGCTTTATTTGGACTTGGCGCAGATAATGTATATATTTAGCAACTTTGCACTATGTAAAGTACCTTATAT  
 ATTGCACTTTAAATTTCTCTCCTGATGGGTACTTTAATTTGAAATGCACTTTATGGACAGTTATGTCTTATAAC  
 TTGATTGAAAATGACAACCTTTTTGCACCCATGTACAGAATACTTGTACGCATTGTTCAAACCTGAAGGAAATT  
 TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATTGAGAGAAGAAGAAGGTGATAAGTGTTGA  
 AAATTAATGTGATAACCTTTGAACCTTGAATTTTGGAGATGTATTCCCAACAGCAGAATGCAACTGTGGGCAT  
 TTCTTGTCTTATTTCTTTCCAGAGAACGTGGTTTTTCATTTATTTTTCCCTCAAAAGAGAGTCAAATACTGACAG  
 ATTCTGTTCTAAATATATTGTTTCTGTCAAAAATTATTGTGATTTCCCTGATGAGTCATATTACTGTGATTTTCA  
 TAATAATGAAGACACCATGAATATACTTTTTCTTCTATATAGTTTCAGCAATGGCCTGAATAGAAGCAACCAGGCA  
 CCATCTCAGCAATGTTTTCTCTGTTTGTAAATTATTGCTCCTTTGAAAATTAAATCACTATTAATTACATTAA  
 AAATCAAATTGGATAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 202**

MTSKFILVSFILAALSLSTTFSLQLDQQKVLLVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK  
QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEEATPIW  
ITNQ RAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY  
WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER  
LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALHAHPNLTVYKKEDVPERWHYKYN  
SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD  
LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF  
IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

**Signal Peptide:**

amino acids 1-22

**Transmembrane Domain:**

amino acids 429-452

**N-glycosylation sites:**

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

**Somatomedin B Domain:**

amino acids 69-85

**Sulfatase protein Region:**

amino acids 212-241

**FIGURE 203**

GGATTTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAGTGCGGGAGGCCCCAG  
GACAGGCCCCACCCTGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGC  
AGAGAGGCCAAGCCCCCTTGCCCTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA  
CCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGCAGGGCC  
AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCGTGGGAGACGA  
CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGG  
AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCC  
CCTGCCCCCTGGCCCCGCACCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT  
CAGCTCCCACAGGTTTCAGGTCATCATCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGC  
TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG  
GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT  
ATTTGTCTTCCGCCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG  
TGGTCTCATTCATCCTGGACATTGTCCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC  
CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT  
TAAGACACGTTTCAAGACGGCAACTCTTAAGGTTAAAACAGATGAATGTACAATTGGCCGCCA  
AGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCTGGACTGATGAGTTTGCTGTATC  
AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT  
CACACAGCCACCGTGAAAGTCCTGGAGTAAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG  
CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA  
TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC  
AAAATCTATAAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 204**

MATWDEKAVTRRAKVAPAERM SKFLRHFTVVGDDYHAWNIN YKKWENEEEEEEEEQPPPTPV  
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILD  
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLSSTTSLRSWMPVVVVVSFILD  
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS  
CSEKPLD



**FIGURE 205**

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCCAGCAGGCCGCCAAC**AT**  
**G**CTCTGTCTGTGCCTGTACGTGCCGGTCATCGGGGAAGCCCAGACCGAGTTCCAGTACTTTG  
 AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCCTCC  
 CAGGAATTCTCCACCTACCGCCAGTGGGAAGCAGAAAATTGTACAAGCTGGAGATAAGGACCT  
 TGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAAGATCATGAGAAGAAGCTGA  
 GGCTGGTGTTTAAGATTTTGGACAAAAGAATGATGGACGCATTGACGCGCAGGAGATCATG  
 CAGTCCCTGCCGGGACTTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATTCTCAAGAG  
 CATGGATAAAAACGGCACGATGACCATCGACTGGAACGAGTGGAGAGACTACCACCTCCTCC  
 ACCCCGTGGAAAACATCCCCGAGATCATCCTCTACTGGAAGCATTCCACGATCTTTGATGTG  
 GGTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCAGACGGGGATGTGGTG  
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGGCCGTATCCAGAACCTGCACGGCCCCCTGG  
 ACAGGCTCAAGGTGCTCATGCAGGTCCATGCCTCCCGCAGCAACAACATGGGCATCGTTGGT  
 GGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGGCAATGGCATCAA  
 CGTCTCAAATTTGCCCCGAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC  
 TTGTTGGTAGTGACCAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCTTGGCA  
 GGGGCCATCGCCCAGAGCAGCATCTACCCAATGGAGGTCTGAAGACCCGGATGGCGCTGCG  
 GAAGACAGGCCAGTACTCAGGAATGCTGGACTGCGCCAGGAGGATCCTGGCCAGAGAGGGGG  
 TGGCCGCTTCTACAAAGGCTATGTCCCCAACATGCTGGGCATCATCCCCTATGCCGGCATC  
 GACCTTGCAGTCTACGAGACGCTCAAGAATGCCTGGCTGCAGCACTATGCAGTGAACAGCGC  
 GGACCCCGCGTGTGTGCTCCTGGCCTGTGGCACCATGTCCAGTACCTGTGGCCAGCTGG  
 CCAGCTACCCCTGGCCCTAGTCAGGACCCGGATGCAGGCGCAAGCCTCTATTGAGGGCGCT  
 CCGGAGGTGACCATGAGCAGCCTCTTCAAACATATCCTGCGGACCGAGGGGGCCTTCGGGCT  
 GTACAGGGGGCTGGCCCCCAACTTCATGAAGGTCACTCCAGCTGTGAGCATCAGCTACGTGG  
 TCTACGAGAACCTGAAGATCACCTGGGCGTGCAGTGCCTG**TC**AGCGGGGGAGGGCCGCCG  
 GCAGTGGACTCGCTGATCCTGGGCGCAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATG  
 TGCCAACACTAAGCTGTCTCGAGCCAAGCTGTGAAAACCTAGACGCACCCGCAGGGAGGGT  
 GGGGAGAGCTGGCAGGCCCAGGGCTTGTCTGTGACCCCGAGCAGACCCTCCTGTTGGTTCC  
 AGCGAAGACCACAGGCATTCCTTAGGGTCCAGGGTCAGCAGGCTCCGGGCTCACATGTGTAA  
 GGACAGGACATTTTCTGCAGTGCCTGCCAATAGGTGAGCCTTGAGCCTGGAGGCCGGCTTAGT  
 TCTTCCATTTACCCCTTGACAGCCAGCTGTTGGCCAGCGCCCTGCCCTCTGGTCTGCCGTGC  
 ATCTCCCTGTGCCCTCTTGTGCTGCCTGTCTGTGCTGAGGTAAGGTGGGAGGAGGGCTACAG  
 CCCACATCCCACCCCTCGTCCAATCCCATAATCCATGATGAAAGGTGAGGTACAGTGGCCT  
 CCCAGGCCTGACTTCCCAACCTACAGCATTGACGCCAACTTGGCTGTGAAGGAAGAGGAAAG  
 GATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATGCT  
 TGGGAGTGCAAGGGGCTCGGGCTGCCTGGCCTGGCTGCACAGAAGGCAAGTGCTGGGGCTCA  
 TGGTGCTCTGAGCTGGCCTGGACCTGTGAGGATGGGCCCCACCTCAGAACCAAACTCACTG  
 TCCCCACTGTGGCATGAGGGCAGTGGAGCACCATGTTTGAGGGCGAAGGGCAGAGCGTTTGT  
 GTGTTCTGGGGAGGGAAGGAAAAGGTGTTGGAGGCCTTAATTATGGAAGTGTGGGAAAAGGG  
 TTTTGTCCAGAAGGACAAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG  
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCCTGTCCAACC  
 CCAGCAGGGGCGCAGCGGGACCAGCCCCACATTCCACTTGTGTCACTGCTTGGAACTATTT  
 ATTTTGTATTTATTTGAACAGAGTTATGTCCTAACTATTTTATAGATTTGTTTAATTAATA  
 GCTTGTCATTTTCAAGTTCATTTTTTATTCATATTTATGTTTCACTGATTGTACCTTCCC  
 AAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGCCTTGGGCCGCTGCAGTCACAT  
 CTGTCCAGAGAAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGGCCAGAAGGCAGCAGCCCTG  
 GCTCCTTTCTTTGGCAGGTTGGGGAAGGGCTTGGCCCCAGCCTTAGGATTTAGGGTTTGA  
 CTGGGGGCGTGGAGAGAGAGGGGAGGAACCTCAATAACCTTGAAGGTGGAATCCAGTTATTT  
 CTGCGCTGCGAGGGTTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAGTGAAGTGCCTCT  
 CACTGTGAATTTGTGGTGGGCGGGGCTGAGGAGAGGGTGGGGGCTGGCTCCGCTCCCTCC  
 CAGCCTTCTGCTGCCCTTGCTTAACAATGCCGGCCAAGTGGCGACCTCACGGTTGCACTTCC  
 ATTCCACCAGAATGACCTGATGAGGAAATCTTCAATAGGATGCAAAGATCAATGCAAAAATT  
 GTTATATATGAACATATAACTGGAGTCGTCAAAAAGCAAATTAAGAAAGAATTGGACGTTAG  
 AAGTTGTCAATTAAGCAGCCTTCTAATAAAGTTGTTTCAAAGCTGAAAAAAAAAAAAAAAAA  
 AA

**FIGURE 206**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD  
LDGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK  
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW  
WRHLVAGGGAGAVSRTCTAPLDRLKVLMOVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI  
NVLKIAPESAIFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSITPMEVLKTRMAL  
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNS  
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG  
LYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation site.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

**FIGURE 207**

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCC**AT**  
**GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG**  
 CAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC  
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAA  
 ACTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA  
 AAGAAGGCAAAGATGAGCTGTCTGGAGCAGGATGAAATGTTTCAGAGGCCGGACAGCAGTGTTT  
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTCGCGCTGAAAAACGTGCAACTCACAGATGC  
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA  
 AAAGTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG  
 CGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA  
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA  
 TGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAA  
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAG  
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTGCCATCAGCT  
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCTTGGCCACAAAAAAG  
 CATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG  
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA  
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA  
 GACATATTAGAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGAGTGATAAG  
 TAAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT  
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG  
 TAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATTCCA  
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG  
 GGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTTTTTATGATGCTTCCAAAGGTGCCT  
 TGGCTTCTCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA  
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAA  
 AA

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**FIGURE 208**

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI  
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTD  
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD  
QGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESEIKRR  
SHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

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**FIGURE 209**

GAATTTGTAGAAGACAGCGGCGTTGCC**ATG**GCGGCGTCTCTGGGGCAGGTGTTGGCTCTGGT  
GCTGGTGGCCGCTCTGTGGGGTGGCACGCAGCCGCTGCTGAAGCGGGCCTCCGCCGGCCTGC  
AGCGGGTTCATGAGCCGACCTGGGCCCAGCAGTTGCTACAGGAGATGAAGACCCTCTTCTTG  
AATACTGAGTACCTGATGCCCTTTCTCCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC  
CTTGGCATCGACAGATCTGACCCTGGCTGTGCCCATCTGTAACTCTCTGGCTATCATCTTCA  
CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC  
GAGTGCGGGACGCAGCTCTGTGGATCTCGACATACCTGTGTAGTTCCCTTCCCAGAACCCAT  
CTCCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCCTGCCCTTTCCTCTGCAGCTGTTTT  
GCTTCCTTGTGGCCATCAGAGTTCCCTTCCCCTGGACAGTCTGGAGAAAGACAGAGGCTGGG  
GTTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCCTCCAGCCCTGTACCAGCTCCTACT  
GGCATGGCTGAGCTCAGACCCTCCTGATTTCTGCCTATTATCCCAGGAGCAGTTGCTGGCAT  
GGTGCTCACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCCAGGGGC  
AACAGTCTACCCTTTGAGTGGGCGGAACCCACTTCCAGCTCTGCTGCCTCCAGGAAGCCCCT  
GGGCCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTTCCCCCTCTCTGGCCTTAGCTT  
CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAAGAGTGAAAG  
AGTTTTGTAACTTCAAGTGCTGTTTCACTGCTGCGGGGATTTAGCACAGGAGACTCTACGCTCA  
CCCTCAGCAACCTTTCTGCCCCAGCAGCTCTCTTCCCTGCTAACATCTCAGGCTCCCAGCCCA  
GCCACCATTACTGTGGCCTGATCTGGACTATCATGGTGGCAGGTTCCATGGACTGCAGAACT  
CCAGCTGCATGGAAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAAACGGGAGGCCTCTG  
GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGGAACCGAGGGAAGAAGGTGCGTCGGA  
GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTTGCTGCCCCACCCATGAGGTAGGCAG  
AAATCCTCACTGCCAGCCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC  
TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAAACAGACAAAAAAAAAAAAA  
AAA

[illegible][illegible]

**FIGURE 211**

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG  
GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT  
TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT  
TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACC**ATGA**AAGGGCATCCTCG  
TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT  
TCATGGGAAAAATCCTGTGTCAACAGCATTCGCTCTGAATGTCCCTCACATGCCAACACCAG  
CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATAACCAGAATATGT  
TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT  
GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG  
CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTTATG  
AATCTAATGGAACCTCCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACAGTGTGTC  
TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC  
CAACGTCAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAAAACAAGACTCTTGAGGAGTCA  
TCTTTCGAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACT  
TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG  
GGGACTGCTGCCCC**TGA**GGTCTTGGGGCTGCACTTTGCCAGCACCCCATTTCTGCTTCTCTG  
AGGTCCAGAGCACCCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAACTGC  
CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA  
AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 212**

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLETPVR  
LYQNMFCSAENCSEETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE  
CPACYESNGTSCRGKPWKCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK  
TLGGVIFRKFEKANVNSLTPTSAPTTSHNVGSKASLYLLALASLLLRGLLP



**FIGURE 213**

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA  
GGGCTTGCCTCACTGGCCACCCTCCCAACCCCAAGAGCCCAGCCCC**ATG**GTCCCCGCCGCCG  
GCGCGCTGCTGTGGGTCCTGCTGCTGAATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCCTG  
ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGCAG  
CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA  
ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC  
ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA  
GGGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCCAGTGCGACTCCCA  
ATACAGCGGGGAGTTCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG  
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC  
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCTCACCCACAG  
CCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC  
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT  
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGACCTATCAACAATGTC  
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT  
GCCTCTCAGAGCACCACCAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG  
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTTGGAAACGGGTCA  
GGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA  
GACAGAAACCAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCT  
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAAACCTGGAAAA  
CACAA

**FIGURE 214**

MVPAAGALLWVLLLNLGPRAGAQLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRI  
ILEDENDAMADADRLAGPAAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL  
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP  
SPSPTAMPSPEDLRLVLMWPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC  
TYQQPCPNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA  
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

**FIGURE 215**

CCCGGGTCGACCCACGCGTCCGGGGAGAAAGG**ATG**CGCCGGCCTGGCGGGCGCGGTTGGTCCTGCTAGCTGGGGCA  
 GCGGCGCTGGCGAGCGGCTCCCAGGGCGACCGTGAGCCGGTGTAACCGGACTGCGTACTGCAGTGCGAAGAGCA  
 GAACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCT  
 GTCGGGACGACTGTAAGTATGAGTGTATGTGGGTACCGTTGGGCTCTACCTCCAGGAAGGTCACAAAGTGCCT  
 CAGTTCCATGGCAAGTGGCCCTTCTCCCGGTTCTGTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCGTTTCT  
 CAATGGCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACA  
 CCTGTGTGGCCTTCGCCCTGGGTGTCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGAC  
 CTCACAGAGAAAATGGACTACTTCTGTGCCTCCACTGTATCCTACACTCAATCTACCTGTGCTGCGTCAGGAC  
 CGTGGGGCTGCAGCACCCAGCTGTGGTCAGTGCCTTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCT  
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTG  
 GTGTGGTGGCTGGCCTGGTGCTGTGGAACAGCGGCGGCTGCCTCACGTGCGCAAGTGGTGGTGGTCTT  
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCCACCGCTCTTCTGGGTCTGGATGCCCATGCCA  
 TCTGGCACATCAGCACCATCCCTGTCCACGTCCTCTTTTTCAGCTTCTGGAAGATGACAGCCTGTACCTGCTG  
 AAGGAATCAGAGGACAAGTTCAGCTGGAC**TGA**AGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCC  
 GCCCTGCTGGCCTCCCTTCTCCCTCAACCCTTGAGATGATTTTCTCTTTCAACTTCTTGAAGTGGACATGA  
 AGGATGTGGGCCAGAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGG  
 AAGGCCTCCAGCATCTGGGACTCGAGAGTGGGCAGCCCTCTACCTCCTGGAGCTGAAGTGGGGTGGAACTGA  
 GTGTGTTCTTAGCTCTACCGGGAGGACAGCTGCCTGTTTCTCCACCAGCCTCCTCCCCACATCCCCAGCTG  
 CCTGGCTGGGTCTGAAGCCCTCTGTCTACCTGGGAGACCAGGGACCACAGGCCTTAGGGATACAGGGGGTCCC  
 CTTCTGTTACACCCCCACCTCCTCCAGGACACCACTAGGTGGTGTGATGCTTGTCTTTGGCCAGCCAA  
 GGTTACGGCGATTCTCCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTACCCTGACC  
 GTTGGCCTAGCCAGGTTCCAGGAGGCCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCCAGGGCA  
 AGGATCCTGTGCTGTGTGTTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGG  
 TGACAGGGCCGTGAGCATGGGCCTGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTTGT  
 CGGGGAAGAGGTGTGGCTTCAAAGTGTGTGTGTGCAGGGGGTGGGTGTGTAGCGTGGGTTAGGGGAACGTGTG  
 TGCGCGTGCTGGTGGGCATGTGAGATGAGTGAAGTGTGTCCACAGTTGAGAGGTTGGAGCAGGAT  
 GAGGGAATCCTGTCAACATCAATAACTTGTGGAGCGCCAGCTCTGCCAAGACGCCACCTGGGCGGACAGC  
 CAGGAGCTCTCCATGGCCAGGCTGCCTGTGTGCATGTTCCCTGTCTGGTGCCCTTTGCCCCCTCTGCAAAC  
 CTCACAGGGTCCCCACACAACAGTGCCTCCAGAAGCAGCCCTCGGAGGCAGAGGAAGGAAAATGGGGATGGC  
 TGGGGCTCTCTCCATCCTCCTTTTCTCCTTGCCTTCGCATGGCTGGCCTTCCCCTCCAAAACCTCCATTCCCCT  
 GCTGCCAGCCCCTTTGCCATAGCCTGATTTTGGGGAGGAGGAAGGGCGATTTGAGGGAGAAGGGGAGAAAGCT  
 TATGGCTGGGTCTGGTTTCTTCCCTTCCCAGAGGTCTTACTGTTCCAGGTGGCCCCAGGGCAGGCAGGGGCC  
 AACTATGCCTGTGCCCTGGTAAAGGTGACCCCTGCCATTTACCAGCAGCCCTGGCATGTTCTTCCCCACAGG  
 AATAGAATGGAGGGAGCTCCAGAACTTTCCATCCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGT  
 CTCTGCCCTGACCCCTTGTCCCTCTTTGAGGGAGGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTG  
 GCCTGCGCTAGCTTCTTTTGATACTGAAAACTTTAAAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAA  
 TTCCAAGCCTCAAAAAAAAAAAAAAAAAA

**FIGURE 216**

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW  
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSRFLFFQEPASAVASFLNGLASLVMLCR  
YRTFVPASSPMYHTCVAFAWVSLNAWFWSTVFHTRDLDLTKMDYFCASTVILHSIYLCCVR  
TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR  
RLPHVRKCVVVVLLQLGLSLLELLDFPPLFWVLDAAHAIWHISTIPVHVLFSSFLEDDSLYLL  
KESEDKFKLD

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

**N-glycosylation site.**

amino acids 40-44

**N-myristoylation site.**

amino acids 43-49

**CUB domain proteins profile.**

amino acids 285-302

**Amiloride-sensitive sodium channels proteins.**

amino acids 162-186

**FIGURE 217**

GGCCGCCTGGAATTGTGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCGTGA  
CT**ATG**GCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG  
CTGATGGCCGCCTGCTTCACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGAC  
CAACCCAGAGAAGAGCAGCACCAAAGAAACGGAGAGAAAAGAAACCAAAGCCGAGGAGGAGC  
TGGATGCCGAAGTCCTGGAGGTGTTCCACCCGACGCATGAGTGGCAGGCCCTTCAGCCAGGG  
CAGGCTGTCCCTGCAGGATCCCACGTACGGCTGAATCTTCAGACTGGGGAAAGAGAGGCAAA  
ACTCCAATATGAGGACAAGTTCGAAATAATTTGAAAGGCCAAAAGGCTGGATATCAACACCA  
ACACCTACACATCTCAGGATCTCAAGAGTGCACTGGCAAATTC AAGGAGGGGGCAGAGATG  
GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGA  
GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTCATTGAGACTGACATGCAGATCATGG  
TACGGCTGATCAACAAGTTCAATAGTTCCAGCTCCAGTTTGAAGAGAAGATTGCTGCGCTC  
TTTGATCTTGAATATTATGTCCATCAGATGGACAATGCGCAGGACCTGCTTTCCTTTGGTGG  
TCTTCAAGTGGTGATCAATGGGCTGAACAGCACAGAGCCCCTCGTGAAGGAGTATGCTGCGT  
TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCCAGGTGGAGGCCATCGAAGGGGGA  
GCCCTGCAGAAGCTGCTGGTCATCCTGGCCACGGAGCAGCCGCTCACTGCAAAGAAGAAGGT  
CCTGTTTGCAGTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCCTGAAGC  
TCGGGGGGGCTGCAGGTCCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG  
CGCGTGGTCACACTGCTCTACGACCTGGTCACGGAGAAGATGTTGCGCGAGGAGGAGGCTGA  
GCTGACCCAGGAGATGTCCCAGAGAAGCTGCAGCAGTATCGCCAGGTACACCTCCTGCCAG  
GCCTGTGGGAACAGGGCTGGTGCAGATCACGGCCCACCTCCTGGCGCTGCCCGAGCATGAT  
GCCCCTGAGAAGGTGCTGCAGACACTGGGCGTCCTCCTGACCACCTGCCGGGACCGCTACCG  
TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA  
GCCTGGAGCTGCAGGATGGTGAGGACGAGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC  
AGCTTGCTGAAGGAGCTGAGAT**TGA**GGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA  
GGCTGAGGGGTGCCAGCGTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCT  
TGGCCATTAAATGGAAACCTGAAGGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AA

**FIGURE 218**

MAPQSLPSSRMAPLGMLLGLLMAACFTFCLSHQNLKEFALTNPESSTKETERKETKAEEL  
DAEVLEVFHPTHEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGRDLINTN  
TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV  
RLINKFNSSSSSLEEKIAALFDLEYVHQM DNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF  
VLGAAFSSNPVKQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL  
GGLQVLR TLVQEKGTEVLAVRVVTL LYDLVTEKMFAEEEAELTQEMSPEKLQQYRQVHLLPG  
LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLAS  
LELQDGEDEGYFQELLGSVNSLLKELR

**Important features:****Signal peptide:**

amino acids 1-29

**Hypothetical YJL126w/YLR351c/yhcX family protein.**

amino acids 364-373

**N-glycosylation site.**

amino acids 193-197, 236-240

**N-myristoylation site.**

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

**Homologous region SLS1 protein.**

amino acids 68-340

**FIGURE 219**

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCC  
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCCTCGTGGGGTCGCGTTGCCACCCCA  
 CGCGGACTCCCCAGCTGGCGCGCCCCCTCCCATTTGCCTGTCCTGGTCAGGCCCCCACCCTCC  
 TTTCCACCTGACCAGCC**ATG**GGGGCTGCGGTGTTTTTTCGGCTGCACTTTTCGTGCGGTTTCGGC  
 CCGGCCTTCGCGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGT  
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTTCATCTTGG  
 TCCATGTGACCGACCGGTGAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTTGGTGCTGCT  
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGA  
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCT  
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCT  
 GATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCCTGACTTC  
 AGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG  
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCCTGGTGGTTGGGAGTCACCTACTGACATCG  
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCCTGCTGCCATCTATGCAGTCACTGT  
 TTCCATGGGGCTCTGGGCCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTCAGCGCAGCC  
 TCTTGTGTAAGGACT**TGA**CTACCTGGACTGATCGCCTGACAGATCCCACCTGCCTGTCCACTG  
 CCCATGACTGAGCCCAGCCCCAGCCCGGGTCCATTGCCACATTCTCTGTCTCCTTCTCGTC  
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT  
 TACCAGGAGCAGCCTGGGTTGAGCCAGTCAGTGACTGGTGGGTTTGAATCTGCACTTATCCC  
 CACCACCTGGGGACCCCTTGTGTGTCCAGGACTCCCCCTGTGTGAGTGCTCTGCTCTCAC  
 CCTGCCCAAGACTCACCTCCCTTCCCCTCTGCAGGCCGACGGCAGGAGGACAGTCGGGTGAT  
 GGTGTATTCTGCCCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGGGGGGACCCCTGGGC  
 CTGGGGTGCCCTCCTGATGTCCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGACG  
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA  
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC  
 AGGCCTGAGGGGGAACCATTTTTTGGTGTGATAAATACCCTAACTGCCTTTTTTTCTTTTTT  
 GAGGTGGGGGGAGGGAGGAGGTATATTGGAACCTCTTCTAACCTCCTTGGGCTATATTTCTC  
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTTCGGTCCCTTTCTCCTTGGTCCCAGACCTT  
 GGGGGAAGGAAGGAAGTGCATGTTTGGGAAGTGGCATTACTGGAATAATGGTTTTAACCT  
 CCTTAACCACCAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGCTGTGGTGAGCTGGC  
 CACTCCAGAGCTGCAGTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGG  
 GAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGT  
 ATCATTTTCTGCTGAGGGTGGAGTGTCCATCCTTTTAATCAAGGTGATTGTGATTTTGACT  
 AATAAAAAAGAATTTGTAAAAA  
 AA

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**FIGURE 220**

MGA AVFFGCTFVAFGPAFAFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR  
SDARLQYGLLI FGAAVS VLLQE VFRFAYYKLLKKADEGLASLSE DGRSPISIRQMAYVSGLS  
FGIISGVFSVINILADALGPGVVG IHG DSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRR  
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSL LCKD

09493 08280  
T08280" 266T460



**FIGURE 221**

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTTCGTTGAGTGAGGACGGAAGATCAACCCA  
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT  
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC  
TCACCCTATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

**FIGURE 222**

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG  
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG  
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTN  
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTCTGTTATCAATATTTTGGNTGATGCAN  
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCCTATTAATTCCTGAATTCAGCCTTT  
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA  
GAGGAG

**FIGURE 223**

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTTCCCTTTCCCCG  
GGGTCTGGGGTGACATTGCACGGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC  
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCCTGGTCAGGCCCCCACCCTTTCCCACNTG  
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGGTTTCGGCCCGGCCTTCG  
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA  
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC  
CGACCGGTCAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCC  
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA  
GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG  
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTTG  
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

**FIGURE 224**

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCCNTTCCCCGGGG  
TCTGGGGGTGACATTGCACCGCGCCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC  
CAGNTGGCGCGCCCCCTCCCATTTGCCTGTCCTGGTCAGGCCCCCACCCTTCCCACCTGA  
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTCGCGTTCGGGCCCCGGCCTTC  
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGC  
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA  
CCGACCGGTGAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTC  
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT  
AGCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTG  
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT  
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

**FIGURE 225**

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCCAGGAGGAGGCAG  
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC  
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG  
 TGTCTGTGCGTCCTGCACCCACATCTTTCTCTGTCCCCCTCCTTGCCCTGTCTGGAGGCTGCT  
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT  
 CCTTGTGGTTCCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC  
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT  
 CTCGCCAACAAATGATGTTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA  
 GGACCTGGGAGCTGGGGCCGGGGAAGACGCCCGGTGGATGACAGCAGCAGCCGCATCATCA  
 ATGGATCCGACTGCGATATGCACACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC  
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCACTGCAG  
 GAAGAAAGTTTTAGAGTCCGTCTCGGCCACTACTCCCTGTCACCAGTTTATGAATCTGGGC  
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCTGGCTACTCCCACCCTGGCCACTCT  
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTCGTCCCCTAAAGATGTCAGACCCAT  
 CAACGTCTCCTCTCATTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA  
 CCAAGAGCCCCCAAGTGCACCTCCCTAAGGTCCTCCAGTGCTTGAATATCAGCGTGCTAAGT  
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA  
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC  
 TGCAGGGACTCGTGTCTTGGGGAGATTACCCTTGTGCCCCGGCCCAACAGACCGGGTGTCTAC  
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCC**TG**AGTCAT  
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCA  
 ACCCTCATTCCTTCCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCCTGACCCCATGTCT  
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCCTGG  
 GAACAATTTCCAAAACCTGTCCAGGGCGGGGGTTGCGTCTCAATCTCCCTGGGGCACTTTTCA  
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCCAGAAATAAA  
 CTGAGAAGTGGAAAAAAAAA

**FIGURE 226**

MATARPPMMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSGSNQDLGAGAGEDARSDD  
SSSRIINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS  
PVYESGQQMFQGVKSIHPHGYSHPGHSNDLMLIKLNRRIRPTKDVRPINVSSHCP SAGTKCL  
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGD SGGP  
VVCNGSLQGLVSWGDYPCARPNRPGVYTNLCKFTKWIQETIQANS

**FIGURE 227**

**ATGGTCAACGACCGGTGGAAGACCATGGGCGGGCGCTGCCCAACTTGAGGACCGGGCCGCGCA**  
 CAAGCCGCAGCGGCCGAGCTGCGGCTACGTGCTGTGCACCGTGCTGCTGGCCCTGGCTGTGC  
 TGCTGGCTGTAGCTGTACCCGGTGCCGTGCTCTTCTGAACCACGCCCACGCGCCGGGCACG  
 GCGCCCCACCTGTCGTACGACTGGGGCTGCCAGCGCCAACAGCGCCCTGGTCACTGTGGA  
 AAGGGCGGACAGCTCGCACCTCAGCATCCCTCATTGACCCGCGCTGCCCCGACCTACCGACA  
 GCTTCGCACGCCTGGAGAGCGCCAGGCCTCGGTGCTGCAGGCGCTGACAGAGCACCAGGCC  
 CAGCCACGGCTGGTGGGCGACCAGGAGCAGGAGCTGCTGGACACGCTGGCCGACCAGCTGCC  
 CCGGCTGCTGGCCCGAGCCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCATG  
 GCACGCTGGGCCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGGCCGCTCATCCAGCTTCTC  
 TCTGAGAGCCAGGGCCACATGGCTCACCTGGTGAACCTCCGTGACGACATCCTGGATGCCCT  
 GCAGAGGGACCGGGGGCTGGGCCGGCCCCGCAACAAGGCCGACCTTCAGAGAGCGCCTGCCC  
 GGGGAACCCGGCCCCGGGGCTGTGCCACTGGCTCCCGGCCCGAGACTGTCTGGACGTCTC  
 CTAAGCGGACAGCAGGACGATGGCGTCTACTCTGTCTTTCCACCCACTACCCGGCCGGCTT  
 CCAGGTGTACTGTGACATGCGCACGGACGGCGCGGCTGGACGGTGTTCAGCGCCGGGAGG  
 ACGGCTCCGTGAACCTTCTCCGGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTCACC  
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCTACGAGCT  
 GCACGTGGACCTGGAGGACTTTGAGAATGGCACGGCCTATGCCCCGCTACGGGAGCTTCGGCG  
 TGGGCTTGTTCTCCGTGGACCCCTGAGGAAGACGGGTACCCGCTCACCGTGGCTGACTATTC  
 GGCATGACAGGCGACTCCCTCCTGAAGCACAGCGGCATGAGGTTTACCACCAAGGACCTGA  
 CAGCGACCATTCAGAGAACAACCTGTGCCGCTTCTACCGCGGTGCCTGGTGGTACCGCAACT  
 GCCACACGTCCAACCTCAATGGGCAGTACCTGCGCGGTGCGCACGCCTCCTATGCCGACGGC  
 GTGGAGTGGTCTCCTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG  
 GCCGTCCGGGAGGACCGCT**TAG**ACTGGTGCACCTTGTCTTGGCCCTGCTGGTCCCTGTTCGC  
 CCCATCCCCGACCCACCTCACTCTTTCGTGAATGTTCTCCACCCACCTGTGCCTGGCGGAC  
 CCATCTCCAGTAGGGAGGGGCCGGGCTCCCTGACACGAAGCTCCCTGGGCCGGTGAAGT  
 CACACATCGCCTTCTCGCCGTCCCCACCCCTCCATTTGGCAGCTCACTGATCTCTTGCCTC  
 TGCTGATGGGGCTGGCAAACCTTGACGACCCCAACTCCTGCCTGCCCCACTGTGACTCCGG  
 TGCTGTTTGCCGTCCCCTGGCCAGGATGGTGGAGTCTGCCCCAGGCACCCCTGCCCCGCCC  
 GGCCAAATACCCGGCATTATGGGGACAGAGCAGGGGGCAGACAGCACCCTGGAGTCCCTC  
 CTAGCAGATCGTGGGGAATGTGAGGTCTCTCTGAGGTGAGGTCTGAGGCCAGTATCCTCCAG  
 CCTCCCAATGCCAACCCCAACCCGTTTCCCTGGTGCCAGAGAACCCACCTCTCCCCCAA  
 GGGCCTCAGCCTGGCTGTGGGCTGGGTGGCCCCATCCTACCAGGCCCTGAGGTGAGGATGGG  
 GAGCTGCTGCCTTTGGGGACCCACGCTCCAAGGCTGAGACCAGTTCCCTGGAGGCCACCCAC  
 CCTGTGCCCCGGCAGGCCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCCCACCTGCTCTGT  
 TCTCAAATGAGGCCCAACCCATCCCCACCCAGCTCCCGGCCGTCTCCTACCTGGGGCAGC  
 CGGGGCTGCCATCCCATTCTCCTGCCTCTGGAAGGTGGGTGGGGCCCTGCACCGTGGGGCT  
 GGAAGTGCCTAATGGGAAGCTCTTGGTCTTCTGGGCTGGGGCCTAGGCAGGGCTGGGATGAG  
 GCTTGTACAACCCCCACCACCAATTTCCAGGGACTCCAGGGTCTGAGGCCTCCAGGAGG  
 ATTGACCGTGGCCACCTGGACCCAGGCCAGGCCGGCCGGCGAGTGGTCAAGGGACAGGGA  
 CCACCTCACCGGGCAAATGGGGTGGGGGGGACTGGGGCACCAGACCAGGCACCACTGGACA  
 CTTTCTTGTGAATCCTCCCAACACCCAGCACGCTGTATCCCCACTCCTTGTGTGCACACA  
 TGCAGAGGTGAGACCCGCGAGGCTCCCAGGACCAGCAGCCACAAGGGCAGGGCTGGAGCCGG  
 TCCTCAGCTGTCTGCTCAGCAGCCCTGGACCCGCGTGCGTTACGTGAGGCCAGATGCAGGG  
 CGGCTTTTCCAAGGCCTCCTGATGGGGGGCTCCGAAAGGGCTGGAGTCAGCCTTGGGGAGCT  
 GCCTAGCAGCCTCTCCTCGGGCAGGAGGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA  
 GGTGCCTAGGGGGTGTGGGGTTCGGTTCTCCCTTCCCCTCCCCTGAAGTTTGTGCTTAAAA  
 AACAAATAAATTTGACTTGGCACCACTGGGGGTGGTGGGAGAGGCCGTGTGACCTGGCTCTC  
 TGTCCCAGTGCCACCAGGTCATCCACATGCGCAG

**FIGURE 228**

MVNDRWKTMGGAAQLEDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT  
APPPVVSTGAASANSALVTVERADSSHLNILIDPRCPDLTDSFARLESAQASVLQALTEHQA  
QPRLVGDQEQELDLADQLPRLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL  
SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQRAPARGTRPRGCATGSRPRDCLDVL  
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFVRGWDAYRDGFGRLT  
GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS  
GTAGDSLLKHSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG  
VEWSSWTGWQYSLKFSEMKIRPVREDR



**FIGURE 229**

GCAGTCAGAGACTTCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT  
TGCTTCCTGAACTAGCTCACAGTAGCCCGGCGGGCCAGGGCAATCCGACCACATTTCACTCT  
CACCGCTGTAGGAATCCAG**ATG**CAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG  
ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC  
CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGAC  
TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC  
AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC  
CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGC  
TGAAAAACTCTGTCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG  
AACAAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAG  
GACTGTAAATATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAAGAAGA  
CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT  
TGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTG  
TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG  
GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA  
TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACT**TGA**TTCGCC  
CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT  
TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG  
TTTCCTGTTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA  
AGAAGTCTTATTTACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTG  
GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT  
GTCTTCCTTACACTTGGTGGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC  
ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTACC  
AGCAAATACACAAGGAATCTTTTTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCAT  
CAGTAAAGACCCCATCTGCCTTGTCATGCCGTTTCCCAACAGGGATGTCACCTTGATATGAG  
AATCTCAAATCTCAATGCCTTATAAGCATTCCTTCCTGTGTCCATTAAGACTCTGATAATTG  
TCTCCCCCTCCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG  
AACTACCGTCCCCGATATTCCTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCA  
TCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTTCA  
GTACTGAAGATTTAATAATAATAAATGTAAATACTGTGAAAAA

**FIGURE 230**

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLL  
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE  
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS  
QSYSEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKD  
CKELKRCVCERRAGMVKPESLHVPPETLGEGD

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**FIGURE 231**

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG  
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG  
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG  
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTA  
CTACCAGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATA  
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTNTGCAGCAT  
GTGGCTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAACTTTGAAGGAGGGCAA  
AGTNTCCTCATNTACTATACACACACCACTTCCC

**FIGURE 232**

GCCGAGCGCAAGAACCCTGCGCAGCCCAGAGCAGCTGCTGGAGGGGAATCGAGGGCGCGGCTC  
 CGGGGATTTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGGAGCGGGCCCCGCGGGG  
 CCCGAGCCCTCCGGATCCGCCCCCTCCCCGGTCCCCCCCCCTCGGAGACTCCTCTGGCTGCT  
 CTGGGGGTTTCGCCGGGGCCGGGGACCCGCGGTCCGGGCGCC**ATG**CGGGCATCGCTGCTGCTG  
 TCGGTGCTGCGGCCCCGAGGGCCCCGTGGCCGTGGGCATCTCCCTGGGCTTCACCTGAGCCT  
 GCTCAGCGTCACCTGGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCCAACCTGGAGACTCTG  
 AGGTGCCGCCGCGCGGCAACACCAACGCGGGCGCGCCGCCCCAACTCGGTGCAGCCCGGAGCG  
 GAGCGCGAGAAGCCCCGGGGCCGGCGAAGGCGCGGGGAGAATTGGGAGCCGCGCGTCTTGCC  
 CTACCACCCTGCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTCAGGACCCGCTACATCAGCA  
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCCC  
 ACGCTGGGCGTGGCCGTGAACCGCACGCTGGGGCACCCGGCTGGAGCGTGTGGTGTTCCCTGAC  
 GGGCGCACGGGGCCGCGGGGCCCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC  
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC  
 TGGTTCTTCTGGTGCCTGACACCACCTACACCGAGGCGCACGGCCTGGCACGCCTAACTGG  
 CCACCTCAGCCTGGCCTCCGCGGCCACCTGTACCTGGGCGGGCCCCAGGACTTCATCGCG  
 GAGAGCCCCACCCCGGCCGCTACTGCCACGGAGGCTTTGGGGTGCTGCTGTGCGCATGCTG  
 CTGCAACAACTGCGCCCCCACCTGGAAGGCTGCCGCAACGACATCGTCAGTGCGCGCCCTGA  
 CGAGTGGCTGGGTGCGTGCATTCTCGATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGG  
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGGAGCCAGTGACAGAGGGGGACCCTCAT  
 TTCCGAAGTGCCCTGACAGCCACCCCTGTGCGTGACCCTGTGCACATGTACCAGCTGCACAA  
 AGCTTTTCGCCCCGAGCTGAACTGGAACGCACGTACCAGGAGATCCAGGAGTTACAGTGGGAGA  
 TCCAGAATAACAGCCATCTGGCCGTTGATGGGGACCGGGCAGCTGCTTGGCCCGTGGGTATT  
 CCAGCACCATCCCGCCCGGCCCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA  
 GCACGCTTTCTCTCTGCGCCGATGGCTCACCCCGCTGCCCCTGCGTGGGGCTGACCGGGCTG  
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCCGCTACCACCCGGCCTTG  
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCCGGGGTATGGA  
 ATACACGCTGGACTTGACAGCTGGAGGCACTGACCCCCAGGGAGGCCGCGGCCCTCACTC  
 GCCGAGTGCACTGCTCCGGCCGCTGAGCCGCGTGGAGATCTTGCCCTGTGCCCTATGTCACT  
 GAGGCCTCACGTCTCACTGTGCTGCTGCCTCTAGCTGCGGCTGAGCGTGACCTGGCCCCCTGG  
 CTTCTTGGAGGCCCTTTGCCACTGCAGCACTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC  
 TGCTGCTACTGTATGAGCCGCGCCAGGCCAGCGCGTGGCCCATGCAGATGTCTTCGCACCT  
 GTCAAGGCCCACGTGGCAGAGCTGGAGCGGCGTTTCCCCGGTGCCCGGGTGCCATGGCTCAG  
 TGTGCAGACAGCCGCACCCCTCACCACTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCGC  
 TGGACACACTGTTCTCTGCTGGCCGGGCCAGACACGGTGCTCACGCCTGACTTCCTGAACCGC  
 TGCCGCATGCATGCCATCTCCGGCTGGCAGGCCTTCTTTCCCATGCATTTCCAAGCCTTCCA  
 CCCAGGTGTGGCCCCACCACAAGGGCCTGGGCCCCCAGAGCTGGGCGGTGACACTGGCCGCT  
 TTGATCGCCAGGCAGCCAGCGAGGCCTGCTTCTACAACCTCCGACTACGTGGCAGCCCGTGGG  
 CGCCTGGCGGCAGCCTCAGAACAAGAAGAGGAGCTGCTGGAGAGCCTGGATGTGTACGAGCT  
 GTTCCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGGCGCTGCTGCAGCGCT  
 ACCGGGCCCAGACGTGCAGCGCGAGGCTCAGTGAGGACCTGTACCACCGCTGCCTCCAGAGC  
 GTGCTTGAGGGCCTCGGCTCCCGAACCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG  
 CAACAGCACCT**TGA**CCCCACCCTGTCCCCGTGGGCCGTGGCATGGCCACACCCCACTT  
 CTCCCCAAAACAGAGCCACCTGCCAGCCTCGCTGGGCAGGGCTGGCCGTAGCCAGACCCC  
 AAGCTGGCCCACTGGTCCCCTCTCTGGCTCTGTGGGTCCCTGGGCTCTGGACAAGCACTGGG  
 GGACGTGCCCCCAGAGCCACCCACTTCTCATCCCAAACCCAGTTTCCCTGCCCCCTGACGCT  
 GCTGATTGCGGGCTGTGGCCTCCACGTATTTATGCAGTACAGTCTGCCTGACGCCAGCCCTGC  
 CTCTGGGCCCTGGGGGCTGGGCTGTAGAAGAGTGTGTTGGGGAAGGAGGGAGCTGAGGAGGGG  
 GCATCTCCCAACTTCTCCCTTTTGGACCCTGCCGAAGCTCCCTGCCTTTAATAAACTGGCCA  
 AGTGTGGAAAAA

**FIGURE 233**

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP  
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAAKKAVRTRYISTELGIRQRLLVAVL  
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLL  
QHGDDEFDWWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG  
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCIL DATGVGCTGDHEGVHYSHLELSPGEP  
VQEGDPHFERSALTAHPVRDPVHMYQLHKAFARAELETTYQEIQELQWEIQNTSHLAVDGDRA  
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLTGTALEELN  
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI  
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLLYEPRQAQRVA  
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPLRLMDLLSKKHPLDTLFLLAGPDTV  
LPDFLNRCRMHAISGWQAFFPMHFQAFHPGVAPPQGPGPPELGRDTGRFDRQAASEACFYNS  
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL  
YHRCLQSVLEGLGSRTQLAMLLFEQE QGNST

**FIGURE 234**

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT  
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT  
 AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTTAGAAAGCTTGATTTCCCTTTGAAGATGAAAG  
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA  
 CTGTATCCACCCAAATGTCACCGATTTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA  
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG  
 AGGGTTGCTCAACGCCCCGCCTCATTGGAACCAATCAGATCTGGGACCTATATAGCGTG  
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCT  
 TTCCCCGCCCCGTGAGACCCTGCAGCACCATCTGTC**ATG**GCGGCTGGGCTGTTTGGTTTGAGC  
 GCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCCGCGTCCGCTGGGA  
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAAGCGGCCCCCAGAAC  
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGTATGAGAAGAACCCA  
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGTCTGGAACATGCGACTTGTCTTCTT  
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA  
 GGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC  
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**  
**A**CCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCCTGCCTGCCATTCTGAC  
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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**FIGURE 235**

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPE  
DENLYEKNPD SHGYDKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAER  
LVKYREANGLPIMESNCFDPSKIQLPED

00440330 00000000

**FIGURE 236**

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC  
TCCCGGCCGCCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT  
GTGGCGGGAAAGCGGCCCCCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGA  
CGAAACTTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTTGGACG  
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACC  
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT  
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCCAGCA  
AGATCCAG



**FIGURE 237**

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCCTGTTGCTCCTGGGGCCCGGCGGCTGGTGCCT  
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTTGTCATCACCCCGCTGCCTTCCGGGG  
 ACGTAGCCGCCACATTCCAGTTCGCGACGCGCTGGGATTTCGGAGCTTCAGCGGGAAGGAGTG  
 TCCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA  
 GCTGCACCTGTCATTACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCTTCCTGC  
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAA  
 TCTTGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGA  
 CTCCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTG  
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGGAGGTGGTCTGCACCGAAAACCTCACC  
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTCTCTGTGCTGCTGAAGGCAGA  
 TCGCTTGTTCCACACCAGCTACCACTCCCAAGGCAGTGCATATCCGCCCTGTTTGCAGAAATG  
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCAGTTGTATTTGATGCCTTC  
 ATCACGGGGCAGGGAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCCCTCACGGA  
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCACTACAACCAGGACA  
 ACGAGACATTAGAGGTGCACCCACCCCCGACCACTACATATCAGGACGTCATCCTAGGCACT  
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACTCTCGAAACCT  
 CAACATCCAGCTCAAGTGGAAGAGACCCCCAGAGAATGAGGCCCCCCCCAGTGCCCTTCCTGC  
 ATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC  
 AACACCCACCCATAACGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG  
 GCTGTATGTGCACACCCTCACCATCACCTCCAAGGGCAAGGAGAACAACCAAGTTACATCC  
 ACTACCAGCCTGCCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTCAGCTGCCG  
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA  
 CACGCCAGATCCTAACCATGGCTTCTATGTCAGCCCATCTGTCCTCAGCGCCCTTGTGCCCA  
 GCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCCTCTTCAACAGCCTGTTCCCA  
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC  
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT  
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT  
 GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACTCT**TGAT**T  
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTT  
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTCAGGGC  
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGGAATTTGAATTAA  
 CTTAGAAATTCAATTCCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA  
 AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACACAGAAAGGTC  
 GGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGGA  
 TGGAGTTTACTGTTTGTGGAATAAAAACGGCTGTTTCCGTGGAAAAAAAAAAAAA

[illegible][illegible]

**FIGURE 239**

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG  
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCCAGCTGACAACGTACGC  
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGGAAAGGAAGTG  
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCCTGTGAAGGAAGTGAAGAAGGAGGAA  
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC  
TCCTCCTCTACCAGGTGTCCTCAGAAATGATGCTGGGTCCCTTTCTACCTCTGGGGGTCACTC  
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGGAATATGGAAGAAGCAATACCCAACC  
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAAG  
TCCAGACCCCAGGGACGGTACTTTCCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT  
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC  
TGCAATGTGTGATCACAGCTAGAAGGCACTGTCAGAGAAGAGAACTGGTCCTCACCAGATG  
CTGAATCTGCTGGTGCCTTGATCTTGGACTTCCCAGCCTCTAGAACTGTAAGAAATAAATAT  
TTGCTGTTTATAATCCAA

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## **FIGURE 240**

MGSSSFVLVLMVSLVLTSLVAVLVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC  
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

**Signal sequence:**

amino acids 1-19

**N-myristoylation sites:**

amino acids 23-29, 27-33, 32-38, 102-108

**WAP-type 'four-disulfide core' domain signature:**

amino acids 49-63

20250326 16:50

**FIGURE 241**

AAACCTCAGCACTTGCCGGAGTGGCTCATTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGG  
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC  
 TCTAGAACCCGACCCACCACC**ATG**AGGTCTGCCTGTGGAGATGCAGGCACCTGAGCCAAGG  
 CGTCCAGTGGTCTTTGCTTCTGGCTGTCTGGTCTTCTTTCTCTTCGCCTTGCCCTCTTTTA  
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT  
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA  
 TGCAGAGCCAGCGCCAGAGAACAAATGCCCTCAACACACAAACCCAGCCCAAGGCCCACACCA  
 CCGGAGACAGAGGAAAGGAGGCCAACCAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC  
 ACAGCACAGAGGGCAGCATGGAAGAGCCCAGAAAAAGAGAAAACCATGGTGAACACACTGTC  
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC  
 AGGACACAAAGACGACCCAAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG  
 GTGTCAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAGACGCTCATTCCCAAAAGTCA  
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA  
 CAGCAGTCATCCACCTAAGGAGAAGAAACCTCAGGCCACCCACCCCCTGCCCCCTTTCCAG  
 AGCCCCACGACGCAGAGAAACCAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG  
 GGATTTTGAAGAAAAATACAGCTTCGAAATAGGAGGCCTTCAGACGACTTGCCCTGACTCTG  
 TGAAGATCAAAGCCTCCAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCCAACCTCACTCTC  
 TTCCTGGACTCCAGACACTTCAACCAGAGTGAGTGGGACCGCCTGGAACACTTTGCACCACC  
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG  
 TGCCCCAGCAGCAGCTGCTCCTGGCCAGCCTCCCCGCTGGGAGCCTCCGGTGCATCACCTGT  
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACTCCCACATGGGGCCAGGAGATAGACAGTCA  
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC  
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT  
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACTTCCTGGAAGGCAC  
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT  
 TCTGGTTCAGGCACAGACCCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACCTG  
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCTGGA  
 TGGTGGCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC  
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT  
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTTACATAAACCATGACTTCAAGCTGGA  
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCCTGGTC  
 CCGGAAGTGCCAAAGCCAAGAAC**TGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGCCCTGCTC  
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA  
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT  
 GGCAAATGGCTAATTGAGGTTCTGAAGTTCTTCACTACATTGCTGTAGGTCTGAGGCCAGG  
 GATTTTAAATTAAATGGGGTGATGGGTGGCCAATACCACAATTCCTGCTGAAAAACACTCTT  
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAAGAGCCTGGATTTACAGAAACATATAGATCTG  
 GTTTGAATTCCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGTATTACTTAACTTCACTAC  
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGGTCTATACTTGTCTTG  
 TCTTTAAGCTATTTGACAACTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATTGTT  
 GTCCATGGAAAGGCAAATAAATTTTCTACAGTGAAAAA

**FIGURE 242**

MRSCLWRCRHLSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP  
KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW  
KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTQNGGQTRKLTASRTVSEKHQG  
KAATTAKTLIPKSQHRMLAPTGAVSTRTRQKGVTTAVIPPKEKKPQATPPPAPFQSPTTQRN  
QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFLPNLTLFLDSRHF  
NQSEWDRLEHFAPPPFGFMEELNYSLVQKVVTFRFPVPQQQLLLASLPAGSLRCITCAVVGNGG  
ILNNSHMGQEIDSHDYVFERLSGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVP  
LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLHPDFL  
RYMKNRFLRSKTLGDGAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYYDTSW  
KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRP GPGTAKAKN

**Cytoplasmic Domain:**

amino acids 1-10

**Type II Transmembrane Domain:**

amino acids 11-35

**Lumenal catalytic Domain:**

amino acids 36-600

**Ribonucleotide Reductase small subunit Signature:**

amino acids 481-496

**N-glycosylation Sites:**

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

**FIGURE 243**

CGATGCGCGGACCCGGGCACCCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG  
GAGCAGCGAGTGGA AATTGTT CCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT  
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACAACA  
CCAGAGACTGCACCATT CCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT  
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC  
ATGAGAAGTGCCTTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG  
ACAAGAGATTTATTTTTGCAGACAGACTCTTCCATAAGTCCTTTGAGTTTGTATGTTGTTG  
ACAGTTTGCAGATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACCTATTT

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**FIGURE 244**

MRGPGHPLLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNT  
RDCTIPAYYKRCARLLTRLAVSPVCMEDK

09441932.082304  
20220725T1650



**FIGURE 245**

GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCCTGCGGTCCCTTCTCTGGGAGG  
CCCGACCCCGGCCGCGCCCAGCCCCACC**ATG**CCACCCGCGGGGCTCCGCCGGGCCGCGCCG  
CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCCCTGGTGCTGGCCGGCGAGGACTGCCT  
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT  
GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG  
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT  
CCTCTTTGTTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCCCTGTTGCTACCTGT  
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTGAAGGCCAGGAGATTCCAATGACAGGCATC  
CCAGTGACAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC  
TGGCTTCATGTACCCACCTAGTGGTCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC  
CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC  
**TGA**AGGAACCAGCCATGTCTCTGCTGCCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT  
CCTGTACCTGCATCTGGTCCTGGGGGTGGCAGGAGTCCTCCAGCCACCAGGCCCCAGACCAA  
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGGAACAGGAGCTGAACTAGA  
ACTATGAGGGGTTGGGGGGAGGGCTTGGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG  
GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG  
CCAGGAAGGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT  
TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG  
CTAGATTAAAGCTGTAAAGACAAAA

**FIGURE 246**

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYC  
CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQQLQSP  
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP  
YMPPQPSYPGA

**Transmembrane Domains:**

amino acids 10-28, 85-110

**N-glycosylation Site:**

amino acids 38-41

**N-myristoylation Sites:**

amino acids 5-10, 88-93

**FIGURE 247**

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGGCGCAAGGGTGAGGGCGGCCCCAGAA  
 CCCCAGGTAGGTAGAGCAAGAAG**ATGGT**GTTTTCTGCCCCCTCAAATGGTCCCTTGCAACCATG  
 TCATTTCTACTTTCCTCACTGTTGGCTCTCTTAACTGTGTCCACTCCTTCATGGTGTCAAG  
 CACTGAAGCATCTCCAAAACGTAGTGATGGGACACCATTTCCTTGGAATAAAATACGACTTC  
 CTGAGTACGTCACTCCAGTTTCATTATGATCTCTTGATCCATGCAAACCTTACCACGCTGACC  
 TTCTGGGGAACACGAAAGTAGAAATCACAGCCAGTCAGCCCACCAGCACCATCATCCTGCA  
 TAGTCACCACCTGCAGATATCTAGGGCCACCCTCAGGAAGGGAGCTGGAGAGAGGCTATCGG  
 AAGAACCCCTGCAGGTCCTGGAACACCCCCCTCAGGAGCAAATTGCACTGCTGGCTCCCGAG  
 CCCCTCCTTGTGCGGGCTCCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTTCGGAGAC  
 TTTCCACGGATTTTACAAAAGCACCTACAGAACCAAGGAAGGGGAAGTGGGATACTAGCAT  
 CAACACAATTTGAACCCACTGCAGCTAGAATGGCCTTTCCTGCTTTGATGAACCTGCCTTC  
 AAAGCAAGTTTCTCAATCAAAATTTAGAAGAGAGCCAAGGCACCTAGCCATCTCCAATATGCC  
 ATTTGGTGAAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCATTTTGAGTCTGTCAAGATAACC  
 AGAGTGGAGTCAAGGTTTCTGTTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGC  
 ACTGGATGCTGCGGTGACTCTTCTAGAATTTTATGAGGATTATTTTCAGCATACCGTATCCCC  
 TACCCAAACAAGATCTTGCTGCTATTCCTGACTTTTTCAGTCTGGTGTCTATGGAAAACCTGGGA  
 CTGACAACATATAGAGAATCTGCTCTGTTGTTGATGCGAGAAAAGTCTTCTGCATCAAGTAA  
 GCTTGGCATCACAGTGACTGTGGCCCATGAACCTGGCCACCAGTGGTTTGGGAACCTGGTCA  
 CTATGGAATGGTGGAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGGAGTTTGTG  
 TCTGTCACTGTGACCCATCCTGAAGTGAAGTTGGAGATTATTTCTTTGGCAAATGTTTTGA  
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCCTGTGTCTACACCTGTGGAAAATCCTG  
 CTCAGATCCGGGAGATGTTTGTATGATGTTTCTTATGATAAGGGAGCTTGTATCTGAATATG  
 CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAGTGGTATTGTACAGTATCTCCAGAAGCA  
 TAGCTATAAAAAATACAAAAACGAGGACCTGTGGGATAGTATGGCAAGTATTTGCCCTACAG  
 ATGGTGTAAAAGGGATGGATGGCTTTTGCTCTAGAAGTCAACATTCATCTTCATCCTCACAT  
 TGGCATCAGGAAGGGGTGGATGTGAAAACCATGATGAACACTTGGACACTGCAGAGGGGTTT  
 TCCCCTAATAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCACTACATGA  
 AGGGCTCTGACGGCGCCCCGGACACTGGGTACCTGTGGCATGTTCCATTGACATTCATCACC  
 AGCAAATCCAACATGGTCCATCGATTTTTTGCTAAAAACAAAAACAGATGTGCTCATCCTCCC  
 AGAAGAGGTGGAATGGATCAAATTTAATGTGGGCATGAATGGCTATTACATTGTGCATTACG  
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAAGGAACACACACAGCAGTCAGCAGT  
 AATGATCGGGCAAGTCTCATTAACAATGCATTTTCAGCTCGTCAGCATTGGGAAGCTGTCCAT  
 TGAAAAGGCCTTGGATTTTATCCCTGTACTTGAACATGAAACTGAAATTTATGCCCCGTGTTTC  
 AAGGTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGTG  
 GAAACTCAATTCAGGCCTTCCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG  
 GACAGACGAGGGCTCAGTCTCAGAGCAAATGCTGCGGAGTGAACACTACTCTCGCCTGTG  
 TGCACAACTATCAGCCGTGCGTACAGAGGGCAGAAGGCTATTTTCAGAAAGTGGAAGGAATCC  
 AATGGAACTTGAGCCTGCCTGTGACGCTGACCTTGGCAGTGTGTTGCTGTGGGGGCCAGAG  
 CACAGAAGGCTGGGATTTTCTTTATAGTAAATATCAGTTTTTCTTTGTCCAGTACTGAGAAAA  
 GCCAAATTGAATTTGCCCTCTGCAGAACCCAAAATAAGGAAAAGCTTCAATGGCTACTAGAT  
 GAAAGCTTTAAGGGAGATAAAATAAAAACTCAGGAGTTTCCACAAATTTCTTACATCATTGG  
 CAGGAACCCAGTAGGATACCCACTGGCCTGGCAATTTCTGAGGAAAAACTGGAACAACTTG  
 TACAAAAGTTTGAACCTTGGCTCATCTTCCATAGCCACATGGTAATGGGTACAACAAATCAA  
 TTCTCCACAAGAACACGGCTTGAAGAGGTAAAAGGATTCTTCAGCTCTTTGAAAGAAAATGG  
 TTCTCAGCTCCGTTGTGTCCAACAGACAATTGAAACCATGAAAGAAAACATCGGTTGGATGG  
 ATAAGAATTTTGATAAAATCAGAGTGTGGCTGCAAAGTGAAAAGCTTGAACGTAT**GTAAAAA**  
 TTCTCCCTTGCCCGGTTCTGTTATCTCTAATCACCAACATTTTGTGTGAGTGTATTTTCAA  
 ACTAGAGATGGCTGTTTTGGCTCCAACCTGGAGATACTTTTTTCCCTTCAACTCATTTTTTGA  
 CTATCCCTGTGAAAAGAATAGCTGTTAGTTTTTCATGAATGGGCTTTTTTCATGAATGGGCTA  
 TCGCTACCATGTGTTTTGTTTCATCACAGGTGTTGCCCTGCAACGTAAACCCAAGTGTTGGGT  
 TCCCTGCCACAGAAGAATAAAGTACCTTATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 248**

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH  
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLQVLE  
 HPPQEQIALLAPEPLLVLGYTVVIHYAGNLSETFHGFKSTYRTKEGELRILASTQFEPTA  
 ARMAFFCFDEPAFKASFSIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA  
 FIIISDFESVSKITKSGVKVSVYAVDPKINQADYALDAVTLLEFYEDYFSIPYPLPKQDLAA  
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL  
 WLNEGFAKFMFVSVSVTHPELVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD  
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMVG  
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD  
 TGYLWHVPLTFITSKSNMVHRFLLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL  
 TGLLKGTHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP  
 MYKLMEKRDMEVETQFKAFILRLRLDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV  
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALC  
 RTQNKEKLQWLLDESFKGDKIKTQEFQILTLIGRNPVGYPLAWQFLRKNWNKLVQKFELGS  
 SSIAHVMVGTTNQFSTRTRLEEVKGFFSSLKENGSQLRCVQQTETETIEENIGWMDKNFDKIR  
 VWLQSEKLERM

**Signal peptide:**

amino acids 1-34

**N-glycosylation sites:**

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

**Neutral zinc metallopeptidases, zinc-binding region signature:**

amino acids 350-360

**FIGURE 249**

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC  
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC  
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA  
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGCTGCACGG  
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC  
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT  
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCCAGTCTGCTTGTCTATGG  
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACACTGTTATGAT  
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC  
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA  
 ACTGCAATAGGAAAGATTTTCTGACCTGTCATCGGGGGACCACCATTATGACACACGGAAAC  
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT  
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG  
 GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG  
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG  
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCCTGTCCCAGGAGACCGGCAGTGTC  
 CTACCTGTGTGCAGCCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG  
 GGCGCCACTCATTGTTATGATGGGTACATTCATCTCTCAGGAGGTGGGCTGTCCACCAAAT  
 GAGCATTCAAGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGAACCACACCAGACAAATCG  
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT  
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGGCTGGCACTGGCCCCAGCGCTGTG  
 GTGGGGAGTGGTTTGCCCTTCCTGCTAACTCTATTACCCCCACGATTCTTCACCGCTGCTGA  
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC  
 CCATTCTGTCCATGAATCATCTTCCCCACACACAATCATTCATATCTACTCACCTAACAGCA  
 AACTGGGGAGAGCCTGGAGCATCCGGAATTGCCCTATGGGAGAGGGGACGCTGGAGGAGTG  
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

**FIGURE 250**

MSAVLLLALLGFILPLPGVQALLCQFGTVQHVWKVSDLPRQWTPKNTSCDSGLGCQDTLMLI  
ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP  
PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLLRRLRGGGIFSNLRVQGCMPQPGCN  
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL  
LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCNSASSSSVLLN  
SLPPQAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC  
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLESLTWGVGLALAPALWWGVVC  
PSC

**FIGURE 251**

GCGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCCCTGCCTGCGCT  
CAGG**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG  
CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG  
CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAAGAGTCG  
GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTTCGTAT  
GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC  
TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG  
AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTGCGC  
GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA  
CGCCCAGCTGTCCTGCCAGGGCCGCGGGGGCACGCTGAGCATGCCCAAGGACGAGGCTGCCA  
ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCCTGTCTTCATCGGCATCAAC  
GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA  
GTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT  
CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG  
GAGAACATG**TGA**GCCTCAGGCTGGGGCTGCCCATTGGGGGCCCCACATGTCCCTGCAGGGTT  
GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG  
GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG  
AAAGTGTTTCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA  
ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC  
TATACAATAAAATCTTTAAGTAGTGCAAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

**FIGURE 252**

M R G N L A L V G V L I S L A F L S L L P S G H P Q P A G D D A C S V Q I L V P G L K G D A G E K G D K G A P G R P G R V G  
P T G E K G D M G D K G Q K G S V G R H G K I G P I G S K G E K G D S G D I G P P G P N G E P G L P C E C S Q L R K A I G E  
M D N Q V S Q L T S E L K F I K N A V A G V R E T E S K I Y L L V K E E K R Y A D A Q L S C Q G R G G T L S M P K D E A A N  
G L M A A Y L A Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T F N K W R S G E P N N A Y D E E D C V E M V A S  
G G W N D V A C H T T M Y F M C E F D K E N M

094193 03230 266T4660



**FIGURE 253**

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG  
CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCCTAGCCAGTTCCTTGATCCTGCCAGACCACC  
CAGCCCCCGGCACAGAGCTGCTCCACAGGCACC**ATG**AGGATCATGCTGCTATTACAGCCAT  
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG  
TTCCTGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC  
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA  
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA  
GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCC  
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC  
TTTA**TAA**GACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT  
ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC  
TTTCCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGT  
AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA  
TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGT  
CCTACATTAAAAATATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTTGCATATGAA  
AAA

## **FIGURE 254**

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK  
ALSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGK  
SSLGTEEQRPL

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 36-45

**N-myristoylation site.**

amino acids 33-39, 59-65

**Amidation site.**

amino acids 90-94

**Leucine zipper pattern.**

amino acids 43-65

**Tachykinin family signature.**

amino acids 86-92

**FIGURE 255**

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCCGCTGTGCCTGCTGTGCC  
CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG  
GAGCCCTGCGGAGAGCTCAAGCGCCCAGCTCTGCCCCAGGAGCCCAGGCTGCCCCGTGAGTC  
CCATAGTTGCTGCAGGAGTGGAGCC**ATG**AGCTGCGTCCTGGGTGGTGTCATCCCCTTGGGGC  
TGCTGTTCTGCTGCGGATCCCAAGGCTACCTCCTGCCCCAACGTCACCTCTCTTAGAGGAG  
CTGCTCAGCAAATACCAGCACAACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGA  
GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT  
CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCGGGGGTGGGGC  
CTGGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGG  
CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTT  
TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCATGCCCTG  
AAACCT**TAG**ACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAG  
GCATGCACCATGGTGCCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGT  
TGCCCAGGCTGGTCTTGAACTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG  
CTAGGATTATAGGCATGAGTCACCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA  
ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC  
TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGGCCAGGG  
CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC  
CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCTTCCTCGCGTGGTTGCCATGACT  
GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGG  
CTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCTCCCGGGT  
GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG  
TGGAACCTTCCTTCCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAGG  
GTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCAGCTATGAATGGCTT  
TTTAAACAAACCCACGTCCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATC  
CAAGTTAGCCGGGCATGGTGGTGCGCACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAG  
GTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC  
AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAAA

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## **FIGURE 256**

MSCVLGGV IPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML  
HNKLRGQVQPQASNMEYMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR  
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation site.**

amino acids 27-31, 41-45

#### **N-myristoylation site.**

amino acids 126-132, 140-146

#### **Amidation site.**

amino acids 85-89

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**FIGURE 257**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GG  
GTCTGGGCTGCCCCCTTGTCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAACAGGGCCGG  
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGC  
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC  
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG  
TGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT  
CAGCAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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**FIGURE 258**

MGSGPLVLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSGTS  
VTLHHARSQHHVVCNT

094499.02204  
20220.264450

**FIGURE 259**

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT  
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGT  
**TATG**ATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC  
TATTAATATTTACCATTCGAGAAGCTTCATTCAGTGTTGAAAATGAATGCTTAGTGGATCTG  
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCCCTCCC  
CTCCGATTGTTCTAAA**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG  
TATGATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTTT  
TTTTCTTGGCACTAATCAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA  
GTAATAAGAAACCTGTGTTTATTCTCAGGTATTTTAGAAACAACAGCCATCATTTTATTTT  
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT  
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC  
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA  
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGA  
ATAAAAGTTCATATCTACCC

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## **FIGURE 260**

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLP  
SDCSK

**Important features:**

**Signal peptide:**

amino acids 1-29

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**FIGURE 261**

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACCGGAGCCCTTGAGACATCCTT  
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGG**ATG**ATGGTGGCCCTT  
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCTTGCAGCTTTTCTGCCCCCGCCGAGTGTAC  
 CCAGGACCCAGCCATGGTGCATTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG  
 AAAAAATGTACCCAAGCAACGAGGGCATAACATTCAAGAATTCCAAGAGTTCTCAAAAAATATA  
 TCTGTCATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT  
 GGCAGTGAAGATTGAACGTGCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGCTG  
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA  
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC  
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA  
 ACTCTCCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAC  
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTC  
 CTGGCAGGGAAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTTCATAACCAAGCAACTT  
 CTAATGAGATAATCAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA  
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT  
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTTGGTTCTCA  
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTGATGGGATACCCCATGCAGAAGCCAG  
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGGTTCTCTATGTGGTCTACAGTACTGGGGGCCA  
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC  
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT  
 AAGCAGCTCTATGCCTGGAATGAAGGAAACCAGATCATTTACAAACTCCAGACAAAGAGAAA  
 GCTGCCTCTGAAG**TAA**TGCATTACAGCTGTGAGAAAGAGCACTGTGGCTTTGGCAGCTGTTC  
 TACAGGACAGTGAGGCTATAGCCCCTTCACAATATAGTATCCCTCTAATCACACACAGGAAG  
 AGTGTGTAGAAGTGGAATACGTATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTC  
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTTCAACAATGTCCATTACTCCCCAAA  
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTTGTCTTTACT  
 GCTCCCCAGCATTTACTGTAACCTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC  
 CCCTAATATTCACCACTGGCTTTTCTCTCCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTTT  
 CAAATGTCTATTGATATTCTCCCATTTTCACTGCCCACTAAAATACTATTAATATTTCTTT  
 CTTTTCTTTCTTTTTTTTTTGAGACAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACCTC  
 AGAGCTCAAGAGATCCTCCTGCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC  
 CACACCTGGCTTAAAATACTATTTCTTATTGAGGTTTAACCTCTATTTCCCCTAGCCCTGTC  
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAATATTAACATTTGAATATCGCTTT  
 CCAGGTGTGGAGTGTGTCACATCATTGAATTCTCGTTTACCTTTGTGAAACATGCACAAG  
 TCTTTACAGCTGTCATTCTAGAGTTTAGGTGAGTAACACAATTACAAAGTGAAAGATACAGC  
 TAGAAAATACTACAAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAAATACGTATGTT  
 TGTTCACCTACTCTTATAGTCAATGCGTTCATCGTTTCAGCCTAAAAATAATAGTCTGTCCC  
 TTTAGCCAGTTTTTCATGTCTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATTCCTCC  
 AGAAAACCAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTTGTCTTGCTGTCTCTGT  
 TTCTCTCTTTCTGCTTTAAATTCAATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

**FIGURE 262**

MMVALRGASALLVLFLAAFLPPPQCTQDPAMVHYIYQRFVRVLEQGLEKCTQATRAYIQEFQE  
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL  
QEAEKKKIRTLLNASCDNMLMGIKSLKIVKKMMDTHGSWMKDAVYNPKVYLLIGSRNNTV  
WEFANIRAFMEDNTKPAPRKQILTLSWQGTGQVIYKGFLFFHNQATSNEIIKYNLQKRTVED  
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLTKEPGTLGVEHSWDT  
PCRSQDAEASFLLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH  
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

**FIGURE 263**

GGGCGCCCGCGTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA  
TGTCGGAGCTCATGGGGCTGTCGGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCG  
GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGCCGGCCCGCCTGCCAAAAAGC  
AAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTC  
GGAAGGAGAAGCCTCAACAACACAACCTTCACCCACCGCCTCCTGGCTGCAGCTCTGAAGAGC  
CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGC  
AGATGATCGCACCATCCGCATCTGGAGCACCAGGACTTCCTGCAGCGAGAGCACCAGCA  
TGAGAGCCAACGTGGAGCTGGACCACGCCACCCTGGTGCCTTCAGCCCTGACTGCAGAGCC  
TTCATCGTCTGGCTGGCCAACGGGGACACCCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA  
TGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCCTAAAAAGCACAAGGCGCCTGTCA  
TCGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTC  
CTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACCAGATGAACAACAC  
ACACGCTGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGA  
AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGGAGTTCCAGGAGGTGGTGCAGCCTTCGAA  
CTAAAGGGCCACTCCGCGGCTGTGCACTCGTTTGTCTTCTCCAACGACTCACGGAGGATGGC  
TTCTGTCTCCAAGGATGGTACATGGAACTGTGGGACACAGATGTGGAATACAAGAAGAAGC  
AGGACCCCTACTTGCTGAAGACAGGCCGCTTTGAAGAGGCGGGGGTGGCGCGCGCTGCCGC  
CTGGCCCTCTCCCCAACGCCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCATCTCTA  
CAATACCCGGCGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCA  
ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGGACCGGGCGGTGCCGCTG  
TTTCAACAACACTCCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC  
CTCCAACGAGAGCACC CGCCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCCTGA  
AGAGCCTGGGTGCCCTGAAGAAG**TGA**CTCTGGGAGGGCCCCGGCGCAGAGGATTGAGGAGGAG  
GGATCTGGCCTCCTCATGGCACTGCTGCCATCTTTCCCTCCAGGTGGAAGCCTTTCAGAAGG  
AGTCTCCTGGTTTTCTTACTGGTGGCCCTGCTTCTTCCATTGAACTACTCTTGTCTACTT  
AGGTCTCTCTCTTCTTGTGCTGGCTGTGACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTTC  
CTCCCAGGCCCAGTGGGTGGAATCTGTCCCCACCTGGCACTGAGGAGAATGGTAGAGAGGAG  
AGGAGAGAGAGAGAGAATGTGATTTTTGGCCTTGTGGCAGCACATCCTCACACCCAAAGAAG  
TTTGTAATGTTCCAGAACACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTGCAAGGA  
TGGGAGACTGGGATAGCTTCCCATCACAGAACTGTGTTCCATCAAAAAGACACTAAGGGATT  
TCCTTCTGGGCCTCAGTTCTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTCTTGCA  
AAGATGATATGAGGCTAAGAGAATATCAAGTCCCCAGGTCTGGAAGAAAAGTAGAAAAGAGT  
AGTACTATTGTCCAATGTCATGAAAGTGGTAAAAGTGGGAACCAGTGTGCTTTGAAACCAA  
TTAGAAACACATTCCTTGGGAAGGCAAAGTTTTCTGGGACTTGATCATACTTTTATATGGT  
TGGGACTTCTCTCTTCGGGAGATGATATCTTGTTTAAGGAGACCTCTTTTCAGTTCATCAAG  
TTCATCAGATATTTGAGTGCCCACTCTGTGCCCAAATAAATATGAGCTGGGGATTAAAAAA  
AA

**FIGURE 264**

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQK  
QYQIRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ  
REHRSMRANVELDHATLVRFSPDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK  
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTHAAVSPCGRFVASCQ  
FTPDKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV  
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH  
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQRLQQQLTQ  
AQETLKSLGALKK

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

**Beta-transducin family Trp-Asp repeat protein.**

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

**FIGURE 265**

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG  
 CAGTGTTTTGCCTTCACCCCAAGTGACC**ATG**AGAGGTGCCACGCGAGTCTCAATCATGCTCC  
 TCCTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGT  
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGCTGCGGATGTGCACCCCGCT  
 GGGGCGGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA  
 AGCACACACCTGTCCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGGCAGGTAC  
 CGCTGCTCCATGGACTTGAAGAACATCAATTTT**TAG**GCGCTTGCCTGGTCTCAGGATACCCA  
 CCATCCTTTTCCTGAGCACAGCCTGGATTTTTATTTCTGCCATGAAACCCAGCTCCCATGAC  
 TCTCCCAGTCCCTACACTGACTACCCTGATCTCTCTTGTCTAGTACGCACATATGCACACAG  
 GCAGACATACTCCCATCATGACATGGTCCCCAGGCTGGCCTGAGGATGTACAGCTTGAGG  
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA  
 AATGGCAGAAAGGACATTCCCCCTCCCCTCCCCAGGTGACCTGCTCTCTTTCTGGGCCCTG  
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCCTGGGCACAGGCTCTTGGGT  
 GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGG  
 ACCAATTTGTGGGTAGTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTTAGACCACAGAC  
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA  
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA  
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT  
 TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAAATGCAAATGGTGGTGGTTCAA  
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACTCCTTTCCA  
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG  
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTGAGACCAGGGAGG  
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

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## **FIGURE 266**

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAI SLWLRGLRMCTPLGREGE ECHP  
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINE

**Signal peptide:**

amino acids 1-19

**Tyrosine kinase phosphorylation site:**

amino acids 88-95

**N-myristoylation sites:**

amino acids 33-39, 35-41, 46-52

094493.022201

**FIGURE 267**

AGCGCCCGGGCGTCGGGGCGGTAAAAGGCCGGCAGAAGGGAGGCACTTGAGAAATGTCTTTC  
CTCCAGGACCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC  
TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG  
CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA  
GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT  
CCTCTGTCGAGAGGAAGCTGCGGATCTGTCCTCCCTGAAAAGCATGTTGGACCAGCTGGGGC  
TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT  
TTCAAAGGAGAAATCTTCCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGGCGGAAGAT  
GATGTTTATGGGATTTATCCGTCTGGGAGTGTGGTACAACCTTCTTCCGAGCCTGGAACGGAG  
GCTTCTCTGGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA  
GGAAAGCAGGGCATTCTTCTTGAGCACCGAGAAAAAGAATTTGGAGACAAAGTAAACCTACT  
TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCTCAGAGAAAAAATGAT  
TGTGTGAAACTGCCCAGCTCAGGGATAACCAGGGACATTCACCTGTGTTTCATGGGATGTATT  
GTTTCCACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTA  
TTAATGTATTTTAATATTCTGTTTAGGCCCACTAAGGCAAAATAGCCCCAAAACAAGACTGA  
CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA  
TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG  
TGAGCAAGTCACTTGAGGTCGGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCCGTC  
TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG  
GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA  
CACCCTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

**FIGURE 268**

MSFLQDPSFFTGMWWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTLEKEPR  
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF  
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGFILGGVFV  
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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**FIGURE 269**

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCG  
GGCCAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA  
AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCC**ATG**GCGAACCCCGGGCTGGGGCTG  
CTTCTGGCGCTGGGCCTGCCGTTCTTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA  
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCCAGCTCCGATG  
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG  
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG  
CACCTACCGGCCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG  
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATC**TAG**GTCCCCTCTCCTGCATCTGTCTCC  
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG  
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG  
GCTATTCACCTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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**FIGURE 270**

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV  
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

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**FIGURE 271**

AATATATCATCTATTTATCATTAAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT  
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTTTCTGTCACTATTATTATTGTTG  
GTATGTGAAGCTATTTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT  
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC  
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA  
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG  
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA  
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT  
TTATTAATTTTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA  
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTTACAGAATTGACATTTTAA  
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA  
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

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**FIGURE 272**

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK  
GIVKGRNLDSRGLILGAEAWGRGVKKNT

103230 2661450

**FIGURE 273**

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTTATTTCAGAGGTTTTGTTTTCTCTTAGTTCT  
 GTGCCTGCTGCACCAGTCAAATACTTCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATA  
 TTGTCATTGTTATAGATCCTAGTGTGCCAGAAGATGAAAAAATAATTGAACAAATAGAGGAT  
 ATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGATTTTTTTTCAAAAA  
 TGTATCTATATTAATTCCTGAGAATTGGAAGGAAAATCCTCAGTACAAAAGGCCAAAACATG  
 AAAACCATAAACATGCTGATGTTATAGTTGCACCACCTACACTCCCAGGTAGAGATGAACCA  
 TACACCAAGCAGTTCACAGAATGTGGAGAGAAAGGCCGAATACATTCACCTTCACCCCTGACCT  
 TCTACTTGGAAAAAAACAAAATGAATATGGACCACCAGGCCAAACTGTTTGTCCATGAGTGGG  
 CTCACCTCCGGTGGGGAGTGTTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTGCTAAG  
 TCAAAAAAATCGAAGCAACAAGGTGTTCCGCAGGTATCTCTGGTAGAAATAGAGTTTATAA  
 GTGTCAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAATTGATTCTACAACAAAACCTGTATG  
 GAAAAGATTGTCAATTCCTTTCCTGATAAAGTACAAACAGAAAAAGCATCCATAATGTTTATG  
 CAAAGTATTGATTCTGTTGTTGAATTTTGTAAACGAAAAAACCCATAATCAAGAAGCTCCAAG  
 CCTACAAAACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAATTCCTGAGGATT  
 TTAAAAACACCATAACCCATGGTGACACCACCTCCTCCACCTGTCTTCTCATTGCTGAAGATC  
 AGTCAAAGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAGGACCGCCT  
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACTGTTGAAAAATGGATCCTGGG  
 TGGGGATGGTTCACTTTGATAGTACTGCCACTATTGTAAATAAGCTAATCCAATAAAAAAGC  
 AGTGATGAAAGAAACACACTCATGGCAGATTACCTACATATCCTCTGGGAGGAACCTCCAT  
 CTGCTCTGGAATTAATATGCAATTTTCAGGTGATTGGAGAGCTACATTCCCAACTCGATGGAT  
 CCGAAGTACTGCTGCTGACTGATGGGGAGGATAACACTGCAAGTTCTTGTATTGATGAAGTG  
 AAACAAAGTGGGGCCATTGTTCAATTTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAAT  
 AGAGATGAGCAAGATAACAGGAGGAAGTCATTTTTATGTTTCAGATGAAGCTCAGAACAATG  
 GCCTCATTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGAACTCCCTT  
 CAGCTCGAAAGTAAGGGATTAACACTGAATAGTAATGCCTGGATGAACGACACTGTCATAAT  
 TGATAGTACAGTGGGAAAGGACACGTTCTTTCTCATCACATGGAACAGTCTGCCTCCCAGTA  
 TTTCTCTCTGGGATCCCAGTGGAAACAATAATGGAAAATTTACAGTGGATGCAACTTCCAAA  
 ATGGCCTATCTCAGTATTCCAGGAAGTGCAAAGGTGGGCACTTGGGCATACAATCTTCAAGC  
 CAAAGCGAACCAGAAACATTAACATTTACAGTAACCTTCTCGAGCAGCAAAATCTTCTGTGC  
 CTCCAATCACAGTGAATGCTAAAATGAATAAGGACGTAAACAGTTTCCCCAGCCCAATGATT  
 GTTTACGCAGAAATTCTACAAGGATATGTACCTGTTCTTGGAGCCAATGTGACTGCTTTTCAT  
 TGAATCACAGAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGCAGGCGCTGATT  
 CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAATGGCAGATAT  
 AGCTTAAAGATTTCGGGCTCATGGAGGAGCAAAACACTGCCAGGCTAAAATTACGGCCTCCACT  
 GAATAGAGCCGCGTACATACCAGGCTGGGTAGTGAACGGGGAAATTGAAGCAAACCCGCCAA  
 GACCTGAAATTGATGAGGATACTCAGACCACCTTGGAGGATTTACAGCCGAACAGCATCCGGA  
 GGTGCATTTGTGGTATCACAAGTCCCAAGCCTTCCCTTGCCTGACCAATACCCACCAAGTCA  
 AATCACAGACCTTGATGCCACAGTTTCATGAGGATAAGATTATTCTTACATGGACAGCACCAG  
 GAGATAATTTTGTGTTGGAAAAGTTCAACGTTATATCATAAGAATAAGTGCAAGTATTCTT  
 GATCTAAGAGACAGTTTTGATGATGCTCTTCAAGTAAATACTACTGATCTGTACCAAAGGA  
 GGCCAACTCCAAGGAAAGCTTTGCATTTAAACCAGAAAATATCTCAGAAAGAAAATGCAACCC  
 ACATATTTATTGCCATTTAAAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACATT  
 GCACAAGTAACTTTGTTTATCCCTCAAGCAAATCCTGATGACATTGATCCTACACCTACTCC  
 TACTCCTACTCCTACTCCTGATAAAAGTCATAATTTCTGGAGTTAATATTTCTACGCTGGTAT  
 TGTCTGTGATTGGGTCTGTTGTAATTGTAACTTTATTTTAAAGTACCACCATT**TGA**ACCTTA  
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTTAAAAAACAAAACAAATGTAAGT  
 AAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAAACTCATAAAAAATAATT  
 TTAAGATGTGCGAAAAGGATACTTTGATTAAATAAAAAACTCATGGATATGTAAAAACTGT  
 CAAGATTAATAATTTAATAGTTTCATTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAAC  
 AAAGATCCTTTTTCTACTGATACCTGGTTGTATATTATTTGATGCAACAGTTTTCTGAAAT  
 GATATTTCAAATTTGCATCAAGAAATTAAATCATCTATCTGAGTAGTCAAAATACAAGTAAA  
 GGAGAGCAAATAAACAAACATTTGGAAAAA  
 AA

**FIGURE 274**

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTY  
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC  
 GEKGEYIHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR  
 CSAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE  
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLV  
 LDKSGSMGGKDRLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM  
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTDGEDNTASSCIDEVKQSGAIVH  
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT  
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSGTIMENFTVDATSKMAYLSIPG  
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNKDVNSFPSPMIVYAEILQG  
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNMGVYSRYFTAYTENGRYSLKVRAGH  
 GANTARLKLRPPLNRAAYIPGWVVNGEIEANPPRPEIDEDTQTTLEDFSRASGGAFVVSQV  
 PSLPLPDQYPPSQITDLDATVHEDKIIILTWTA PGDNFVDVGKVQRYIIRISASILDLRDSFDD  
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP  
 QANPDDIDPTPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

CTCCTTAGGTTGGAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAGACCATACGTCCTCCG  
GGCAGGGGTGACAACAGGTGTCATCTTTTTGATCTCGTGTGTGGCTGCCTTCTATTTCAAGGAAAG  
ACGCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACC  
CCCAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTT  
GTGGTTGGAGGAGAAACCTTTGTGGGGCTGCGTTTCTCTTAGCAGTGCTCAGAAGTGAAGTGCCTGA  
GGGTGGACCAGAAGAAAGGAAAGGTCCTTCTGTGCTGTGGCTGCACATCAGGAAGGCTGTGATGGG  
AATGAAGGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCTTTAA  
GTAGAGAAGTGTCTGTGTGGTGGTTAACTTCAAGAGGCAAGTCTGTTCTAGAAGGAAATGGATG  
CAAGCAGCTCCGGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCAGGGAAGCCCTTCCGTGGG  
GCCCCGGCTTTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCTCTGAATGATGATGGTTCGCC  
GGGGGCTGCTTGCCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGTCTCTCTGTCTGTCTGTCTGT  
CCTGTACATGTTGGCCTGCACCCCAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGCCAAACAGC  
CCCACGGGGAAGGAGGGGTACCAGGCCGTCCTTCAGGAGTGGGAGGAGCAGCACCGCCAACTACGTGA  
GCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGGAA  
TGGGCAGTACCAAGCCAGCGATGCTGCTGGCTGGTCTGGACAGGAGGCCCCCAAGAGAAAACCCAG  
GCCACCTCTTGGCTTCTGCTGCTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGG  
CCACAGAGTATGCAGCAGTGCCTTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGG  
CCTTACCCGCCACCCCGAGGAGAAGCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGGAAGCCATT  
GAATCAGCCTTGGAGACCTTGAACATCTTGACAGAGAACGCCCAATCACGCTCCTTACACGGCCT  
CTGATTTTCATAGAAGGGATCTACCGAACAGAAAAGGACAAAGGGACATTGTATGAGCTCACCTTCAA  
AGGGGACCACAAACACGAATTCAAACGGCTCATCTTATTTTCGACCATTACGCCCCATCATGAAAGTG  
AAAAATGAAAAGCTCAACATGGCCAAACACGCTTATCAATGTTATCGTGCCTCTAGCAAAAAGGGTGG  
ACAAGTTCCGGCAGTTCATGCAGAATTTCAGGAGATGTGCATTGACAGGATGGGAGAGTCCATCT  
CACTGTTGTTTACTTTTGGGAAAGAAATAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAA  
GCTGCCAACTTCAGGAACCTTTACCTTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGGACTTG  
ATGTTGGAGCCCGCTTCTGGAAGGGAAGCAACGCTCCTTCTCTTTTCTGTGATGTGGACATCTACTT  
CACATCTGAATTCCTCAATACGTGTAGGCTGAATACAGCCAGGGAAGGAAGGATTTTATCCAGTT  
CTTTTCAGTCAGTACAATCTTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGAACAGC  
AGCTGGTCATAAAGAAGGAAACTGGATTTTGGAGAGACTTTGGATTTGGGATGACGTGTAGTATCG  
GTCAGACTTCATCAATATAGGTGGTGTGATGTGCACATCAAAGCTGGGCGGAGAGGATGTGCAC  
CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACC  
TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGAGCAGTACAAGATGTGCATGCAGTCCAA  
GGCCATGAACGAGGCATCCACCGCCAGCTGGGCATGCTGGTGTCAGGCACGAGATAGAGGCTCAC  
CTTCGCAAAACAGAAAAGCAAGTAGCAAAAAAACA**TGA**ACTCCAGAGAAGGATGTGGGAGA  
CACTTTTTCTTTCTTTTGCAATTACTGAAAGTGGCTGCAACAGAGAAAAGACTTCCATAAAGGACG  
ACAAAAGAATTGGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTGTGGGCTTTTTTAC  
AACAGAAATCAAAATCTCCGCTTTGCTGCAAAAGTAAACCCAGTTGCACCTGTGAAGTGTGACA  
AAGGCAGAATGCTTTGTGAGATTATAAGCCTAATGGTGTGGAGTTTTGATGGTGTTTACAATACACT  
GAGACCTGTTGTTTTGTGTGCTCATTTGAAATATTCATGATTTAAGAGCAGTTTTGTAAAAAATTCAT  
TAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGAGCCTATCAGCAGGGCTCTAGTTCTAGG  
AATGCTAAAATATCAGAAGGCAGGAGGAGATAGGCTTATATGATAGTGTGAGTACATTAAAGTA  
AAAAAATGACACAGAAAAGAAAAGAAACCATAAATATCGTGCATATTTTCCCCAAGATTAACCA  
AAAAAATCTGCTTACTTTTGGTGTGCTTTTAACTGTCTCCGTTTTTTTTCTTTTATTTAAAAAT  
GCACTTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACCCTTTGCAAGCCTTACAAGAGA  
GCACAAGTTGGCTACATTTTTATTTTTTAAAGAAGATACTTTGAGATGCATTTAGAGAACTTTCA  
GTTCAAAGCATCAAATTTGATGCCATATCCAAGGACATGCCAAATGCTGATTTCTGTGAGGCACTGAAT  
GTCAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGACGTACAGATACTTTCTCTGAA  
GAGTATTTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGACACTTTCTGCTTTACAGAA  
AAGGAACTCATTAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCATTTTTCTCCTCA  
GAAGTAGGGACCGCTTTCTTACCTGTTTTAAATAAACCAAAGTATACCGTGTGAACCAAACAATCTCT  
TTTCAAAACAGGGTGTCTCCTCCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAATATATATAT  
ATATATATATATTTGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTTTGTCTACAT  
GTTATCCACCCCAAGGCTGGAAGTAAGTGAATTTTTTAAATAAGCAGTTCTACTCAATCA  
CCAAGATGCTTCTGAAAATTTGCATTTTTATACCATTTCAAACTATTTTTTAAAAATAAATACAGTTA  
ACATAGAGTGGTTTCTTCATTTCATGTGAAAATTTATAGCCAGCACCAGATGCATGAGCTAATTTATCT  
CTTTGAGTCTTGTCTTCTGTTTGTCTACAGTAACCTATTGTTTAAAGCTTCAAGAACATTCACAGC  
TGTGGTGTGTTAAAAAATGCATTGTATTGATTGTTGACTGGTAGTTTATGAAATTTAATTTAAACAC  
AGGCCATGAATGGAAGGTGGTATTGCAACAGCTAATAAATATGATTTGTGGATATGAA

**FIGURE 276**

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ  
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL  
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIES  
ALETNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP  
MKVKNEKLNMAN TLIN VIVPLAKRVDKFRQFMQNFREMCIEQDGRVH LTVVYFGKEEINEVK  
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLN TCR  
LNTQPGKKVFYPVLF SQYNPGIIYGHDAVPPLEQQLV I KKETGFWRDFGFGMTCQYRSDFI  
NIGGFDL DIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMQS  
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT



**FIGURE 277**

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGA CTGCCATTCATGCTGAACTCTGTCAACC  
 AGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT  
 ATGCCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA  
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGGT  
 ATCATTCTGGTTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCCTGCTGTTGAGGTGC  
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAC  
 CTGGAATTTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG  
 GATTATTATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT  
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGATGACGCTGAAGAT  
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCTCTGATCCCCTGGACATGAAGGG  
 GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT  
 TGTTCTGCTTCCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCCTGAAATA  
 CCAAGAGCAGATCATATATTTTGTTCACCATTCTTCTTTTGTAAATAAATTTTGAATGTGCT  
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC  
 TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG  
 TAGTTATTGATTTAAGCATTTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTC  
 AAAGACCTAAGGAAAAATAAATTTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT  
 TGAAAATGGATCCTTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAAACAAAAG  
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAATGGAATTACTCATATACAGGGTGGAATT  
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC  
 AATTCTATTTGTTGACCATTTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG  
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 278**

MLWLLFFLVTAIHAE LCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP  
NREATEISHVLLCNVTQRVSFWFVVTDP SKNHTLP AVEVQSAIRMNKNRINNAFFLNDQTL E  
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRK NKEPSEVDDAEDKC  
ENMITIENGIPSDPLDMKGGILM MPS

09490300 26674660

**FIGURE 279**

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG  
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATG**T  
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATAACAGCTCACAGCTCTTTGG  
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC  
 TCGGTTAAAATGCACTTTCTCCAGCTTTGCCCCGTGTTGGGTGATGCTCTAACAGTGACCTGGA  
 ATTTTCGTCCTCTAGACGGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC  
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA  
 TGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA  
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA  
 CGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT  
 AATAGTAATTGTAGTGGTCCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC  
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT  
 GTTTATTTAGAAGACACAGACT**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA  
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT  
 TTTCCAACCAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC  
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTTCA  
 GTGTAAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTTGCCCTTAA  
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC  
 AATTTGTCTGTTACATTTTCTTTTACGTATTTCTTTTAGCAGCACTTCTGCTACTAAAGTTA  
 ATGTGTTTACTCTCTTTTCTTTCCACATTCTCAATTAAAAGGTGAGCTAAGCCTCCTCGGTG  
 TTTCTGATTAACAGTAAATCCTAAATTCAAAGTTAAATGACATTTTTTATTTTTATGTCTC  
 TCCTTAACTATGAGACACATCTTGTTTTACTGAATTTCTTTCAATATTCCAGGTGATAGATT  
 TTTGTCTG

**FIGURE 280**

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT  
WNFRPLDGGPEQFVFYHIDPFQPMSGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ  
VKNPPDVDGVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVIVVVLQHYRKKRWAER  
AHKVVEIKSKEERLNQEKKVSVYLEDTD

**FIGURE 281**

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACC**ATG**AAGTTCTTAGCAGTCCTGGT  
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAAACAGCTGCTCCAGCTG  
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT  
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG  
TAAAGACATTCCAGTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCC**T**  
**G**AGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACTATTCATGCTTCCTGTGATTTC  
ATCCAAC TACTTACCTTGCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA  
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

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**FIGURE 282**

MKFLAVLVLLGVSI FLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTAT  
TAASTTARKDIPVLPKWVGDL PNGRVCP

0944193-02204  
T0220 25TH60

**FIGURE 283**

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC  
CTAGGGGTCTGGATTTGCTGGTTAACAAGATAACCTGAGGGCAGGACCCCATAGGGGA**ATGC**  
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTACGGTGGCCTGGTCCCTCCTTGCCGAGAGA  
GTGTCCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC  
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG  
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG  
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCCCGCCACAGAGTCATCTGCCCAGCTCCT  
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAG**TAA**AACCACAGGCTGG  
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA  
CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTTACCACATTAGCAATTAAAACTGAGAAAT  
GGGCCGGGCACGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT  
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTACTAAAAA  
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG  
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT  
TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

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**FIGURE 284**

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRLQPFVTERTLGKVQRWSGVHTQTGGRAG  
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCWPVGVARGGALCQ

094930330  
"266T460



**FIGURE 285**

GTC**ATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA  
GCGGCCCCCATGGGCGGCCCAGAACTGGCACAGCATGAGGAGCTGACCCTGCTCTTCCATGG  
GACCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA  
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC  
CGGGGCCGGGATGCAGCCCAGGAACTTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA  
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCCAGGCACAGA  
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT  
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC  
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC  
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCC**TGA**ATCTGCCTGGATGGAAGTGA  
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG  
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC  
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA  
CCCTTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 286**

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK  
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK  
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAQQHRLRQ  
IQERLHTAALPA

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**FIGURE 288**

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHKKRRVRDKDGD LKTQIEKLWT  
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ  
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSSQAQ GK  
WSDEACRSSKRYICEFTIPK

0944930830 2654660

**FIGURE 289**

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCCGGGCAGCCGCAGGTTCCCCGCGCGC  
CCCGAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGGCCCTGTCCTGCA  
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAGCCTGTCGCTGCGCTG  
GAGTCGGCGGCGGAGGCCGGGGCCGGGACCCTGGCCAACCCCCTCGGCACCCTCAACCCGCT  
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCCAGAAGT  
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG  
GCCCTGACAGTGTTTGGCTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC  
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCGGGCCCT  
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAA

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**FIGURE 290**

MKLAALLGLCVALSCSSAAFLVGSAPVAQPVAALSAEAGAGTLANPLGTLNPLKLLLS  
SLGIPVNHIEGSQKCVAELGPQAVGAVKALKALLGALTIVFG

0394193.032904  
03290.2557450

**FIGURE 291**

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCACT  
 CCTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCCTG  
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCCTCAGTCGCCAGAGACCCAGCCCC  
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG  
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT  
 GCCAAGGAGACTTCAAACCTTCGGATTTCAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG  
 CAACATGGTCTTCTCTCCATTTGGCATGTCCTTGGCCATGACAGGCTTGATGCTGGGGGCCA  
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCACCAAG  
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCCTCTCCCGCAACCTGGAACCT  
 GGGCCTCTCACAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT  
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCCTATGAATTTTCGCAATGCCTCA  
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAAGAGACTCGGGGGAAAATTCCCAAACCT  
 GTTTGATGAGATTAATCCTGAAACCAAATTAATTCTTGTGGATTACATCTTGTTCAAAGGGA  
 AATGGTTGACCCCATTTGACCCTGTCTTCACCGAAGTCGACACTTTCACCTGGACAAGTAC  
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA  
 TTTTCGTTGTATGTCCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA  
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA  
 TGGCTCAGAAACATGAAAACCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCA  
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCCTTTG  
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA  
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTCAGAAATTAC  
 TGCTTATTCCATGCCTCCTGTCATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG  
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTAT**TAA**ATTCAGG  
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA  
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCCTTTTGTTCTTAAGTATAGGGTGTTCCTC  
 AAATAAATACAGTAGTCCCCACTTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC  
 CTGAAACGGTGGACAGTGCTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT  
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAACAATAATAACAACATTAAGTAAAA  
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA  
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTGGGCAAGGGGAGAATTCA  
 CATCCTGGGTGGGACAGAGCAGGACGATGCAAGATTCCATCCCACTACTCAGAATGGCATGC  
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTTCATTTAATGTTTTTGGACCATGGT  
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA  
 GCATTAAATTGATACATATTTTTTAAAAA

094199.0220  
 0220.266466

**FIGURE 292**

MKVVP S L L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E  
E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I  
K R G L H L Q A L K P T K P G L L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F  
D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P  
V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V V L M E K M G D H L  
A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A  
T G R N L Q V S R V L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K V D R P F H F M I Y E E T S G M L L F  
L G R V V N P T L L



**FIGURE 293**

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCCAGAC**ATG**AG  
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG  
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG  
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTGTTCCC  
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCCA  
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCCGTGTCCTGAGTCCC  
GAGCCCGACCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC  
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA  
TCTACCACCCCCAG**TAG**GGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGG  
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCCAGCAGGCAAA  
AAAAAAAAAAAAAAAAA

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**FIGURE 294**

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL  
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE  
RPRLWVMPNHQVLLGPEEDQDHIYHPQ

403220" 266T4660

**FIGURE 295**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG  
TACCCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACA**ATGA**AACCAACTCAGCTTCCTGC  
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA  
TGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC  
TAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT  
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG  
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC  
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG  
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG  
CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC  
TGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT  
ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGC  
GACGCCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCAGGATT  
TGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGG  
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTTCCAGAGGCCAGT  
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAACCATGTTGGTTA  
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGT**TGAG**AGTTTTGTG  
GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTACCCA  
GTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

**FIGURE 296**

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN  
GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG  
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI  
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYYSPIYGQREFTAGFVQFRVFNNERAAAN  
ALCAGMRVTGCNTEHHCIGGGGYFPEASPOQCGDFSGFDWSGYGTHVGYSSSREITEAAVLL  
FYR

094193-02201  
T02201 2554660

**FIGURE 297**

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC  
CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG  
CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC  
ATGGCGGCATCTGCAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC  
AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAAC  
CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG  
GCATCTAATAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC  
TACACCCAAAACAACAAGTGTTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG  
TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAACCTATGCAT  
TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC  
GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC  
GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA  
ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAAACAATATTCT  
CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA  
AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTGAATAAACATCTGGATCTTATAGACCGT  
TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCT  
GGGGTGGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA  
TGCCATCTGGGCATACAAATAAGAAGTTTGTCACAGCACTCAGGATTTTGGGTATCTTTTGT  
AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA  
CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG  
TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

[illegible][illegible]

**FIGURE 299**

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGGAGCCGG  
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCCAGCG**ATG**GCGACCCTGTGGGGAGGC  
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCGTGCCTGGCGCTTTCCTGTGCTGCTGGC  
 GCAGCTGTCAGACGCCGCCAAGAATTTTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCT  
 ATAAAGAAAATTCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT  
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA  
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA  
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG  
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT  
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG  
 AATATGCACAGCAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGTCTTTGACCGG  
 CATGTTGTCCTCAGC**TAA**TTGGGAATTGAATTCAAGGTGACTAGAAAGAAACAGGCAGACAA  
 CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTTGATTTACCAACT  
 GTTGCTGGAAGATTCAAACTGGAAGCAAAAACCTTGCTTGATTTTTTTTTCTTGTTAACGTA  
 ATAATAGAGACATTTTTTAAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTG  
 TGACTTTTACTAATAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA  
 AGCACTCTCTTTTTTACCACATAGTTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG  
 TTGTTGTTGTTTTTTGTTTGTGTTTTGTTGGTGGGAGAGGGGAGGGATGCCTGGGAAGTGGTT  
 AACAACTTTTTTCAAGTCACCTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT  
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG  
 ACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGTCTGCACTTCATGGTAAACGGGAT  
 CTAAATGCCTGGTGGCTTTTCACAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG  
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG  
 GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT  
 TGCAATAAAGAAATTTTATTTTAAACCCAAGCCTCCCTGGATTGATAATATATACACATTTG  
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTTGAGCTCCAATATGTGCAGCTTTGAACT  
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT  
 TCTTCCTATGTCCTCTTTGGAATGTAACAATAAAAATAATTTTTGAAACATCAA

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**FIGURE 300**

MATLWGGLLRRLGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS  
GHYNNKNI  
QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVTIIIIYLSILGLLLLYMVYLT  
L  
VEPILKRRLEFGHAQLIQSDDDIGDHQPFANAHDVLRARSRSRANVLNKVEYAQQRWKLQVQEQ  
RKSVEFDRHVVL

0949094  
0920 254450



**FIGURE 301**

GCACCTGCGACCACCGTGAGCAGTCATGGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT  
CTGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCCAAGGCCTTCCTGTCCCGCGGGAAGCGG  
CAGGAGCCGCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCA  
CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG  
CATTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTG  
ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTATATATACTGTACATTCTATT  
TAAGGTAAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAA  
TCATTGTCTACATTAAAACCTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA  
AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTAGTTTTACATAAGAATG  
TTTACTCAATGTTTAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTT  
GAACATGGATCTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

**FIGURE 302**

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGRFPPMMHHHQAPSDGQT  
PGARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRIILI  
ILHQ

FOOOO OOOO

**FIGURE 303**

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCCTGGGTGCTCTTCATCTT  
GGATTTGAAAGTTGAGAGCAGC**ATG**TTTTTGCCCACTGAAACTCATCCTGCTGCCAGTGTTAC  
TGGATTATTCCTTGGGCCTGAATGACTTGAATGTTTCCCCGCCTGAGCTAACAGTCCATGTG  
GGTGATTTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT  
AGACTGGACTCTGTCACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA  
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCGCGTACACTTGATGGGGGACATCTTATGC  
AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA  
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG  
AGGAGCCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTTCAGATGGGATGTGTTTTCCAG  
AGCACAGAAGTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA  
GGAGATTGTATTTTCGTTACTACCACAAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG  
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCATCATG  
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT  
GGTGTTCAGAAAACCATTTGTGCTGCATGTCAGCCCGGAAGAGCCTCGAACACTGGTGACCC  
CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC  
TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA  
GAGTTCAGTGAATTCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG  
AAAAACCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATTGTA  
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA  
CCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG  
GAATGCCAAAAACACAGCAAGCCTTT**TGA**GAAGAATGGAGAGTCCCTTCATCTCAGCAGCGG  
TGGAGACTCTCTCCTGTGTGTGTCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTC  
CCAGCTGTCTCCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG  
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC  
CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCCGTT  
GGATCAGACCCTCCTGTGGGCAGGGTTCTTAGTGATGAGTTACTGGGAAGAATCAGAGATA  
AAAACCAACCCAAATCAA

**FIGURE 304**

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG  
EHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGES  
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY  
HKLMSVEYSQSWGHEFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV  
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLLPVLILIVKKT CGNKSSVNSTV  
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR  
SDRNNSLEKKSGGGMPKTQQAF

**FIGURE 305**

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG  
GTTCTACCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG  
AAACTACATTTTGC AAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCC**ATGCA**  
GGATGAAGATGGATAACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG  
GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG  
ATGGTTGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTCATGCAGCGCAATTACCTACAAGA  
TGAGAATGAAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG  
TAAAACAATCAGAACTAAAGGGCACTTTC AAAGGTCATAAATGCAGCCCCCTGTGACACAAAC  
TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTTAACATGGGAAGAGAG  
TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG  
AGTACATCAAAGCCAGGACTCATTTAATTTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT  
GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGGAAGA  
TGGAAGAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG  
AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT  
**TAA**TGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT  
ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

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**FIGURE 306**

MQDEDGYITLNIKTRKPALVSVGPASSSWVRVMALILLILCVGMVVGLVALGIWSVMQRNYL  
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE  
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEEFL  
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

094193-03301  
"25574650"

**FIGURE 307**

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGCGATCCCGG  
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCCGCGCGGGAGCCGGACCGC  
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGCGGAGAA  
GCCCCGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG  
CGGAGGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAGAAGCGGTGGTGGTGGG  
CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCGCG  
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGC  
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG  
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC  
ACTTGCAGCTGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACT  
CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT  
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTTCACACCTGAGTGCA  
AATTCAAAGAATCAGTGTTTGAATAATTATTATGTGACATATTCATCAATGATATACCGTCAG  
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA  
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT  
ACAAGGAGCCATCACTGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC  
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAAC  
**GTAG**CCAGTGAGGGCAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT  
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGG  
CAGAGTTCATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

**FIGURE 308**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498

><subunit 1 of 1, 245 aa, 1 stop

><MW: 27564, pI: 10.18, NX(S/T): 1

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVFSSRVKLFSGSKRRRRRP  
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA  
MNSEGYLYTSELFTEPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVK  
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNGGKSMSHNEST

**N-glycosylation site.**

amino acids 242-246

**Glycosaminoglycan attachment site.**

amino acids 165-169, 218-222

**Tyrosine kinase phosphorylation site.**

amino acids 93-100

**N-myristoylation site.**

amino acids 87-93, 231-237

**ATP/GTP-binding site motif A (P-loop).**

amino acids 231-239

**HBGF/FGF family proteins**

amino acids 78-94, 102-153



**FIGURE 309**

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG  
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG  
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCT  
 CCATTTAGAGTGTAGCAAAGGAAAAACACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTG  
 CCCAGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCCTGTAGATTAC  
 AAGAGTGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAA  
 ACCACGTCTTGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG  
 GAGAGGAGGGAAAGGGGACGTTTTCAATAGGAGGCCAAACTCGAGGGTGGGATCCACTGAGG  
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCACGGGTGGTAACTGGCTGCT  
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG  
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAG  
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCT**ATG**GCGGCGCTGGC  
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCCGGGGGCAGCCGGCCGGTGTGCG  
 CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG  
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCCGCGCGGCCGGACCGCGGCCCGGAGCCTCA  
 GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG  
 ACGGAAGCATCCAGGGCACCCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCT  
 GTGGGCCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC  
 TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCT  
 TTGAGAATTACTACGTCCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC  
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAA  
 GGCAGCTGCCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC  
 ACAGTGTCCCCGAGGCCTCCCCTTCCAGTCCCCCTGCCCC**TGA**AATGTAGTCCCTGGACTG  
 GAGGTTCCCTGCACTCCCAGTGAGCCAGCCACCACCACAACCTGT

**FIGURE 310**

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR  
GPEPQLKGIVTKLFCRQGFYQLQANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY  
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR  
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSPPPAP

**Tyrosine kinase phosphorylation site:**

amino acids 199-207

**N-myristoylation sites:**

amino acids 54-60, 89-95, 131-137

**HBGF/FGF family signature:**

amino acids 131-155

094193-03204  
T02200-265TH50

**FIGURE 311**

**ATG**GCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG  
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGGCTCTGCAACG  
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG  
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT  
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT  
TCAACCTCATAACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTAT  
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT  
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG  
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA  
GTAAAGAAAACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG  
AGAACCATCTTTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAA  
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

**FIGURE 312**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWD RPSASRRRSSPSKNRGLCNGNLVDIFSKVRI FGLKKRRLR  
RQDPQLKGIVTRLYCRQGYYLQMH PDGALDGTKDDSTNSTLFNLI PVGLRVVAIQGVKTGLY  
IAMNGEGYLYPSELF TPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR  
VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

**N-glycosylation site.**

amino acids 100-104, 242-246

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 28-32, 29-33

**Tyrosine kinase phosphorylation site.**

amino acids 199-207

**N-myristoylation site.**

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

**HBGF/FGF family proteins.**

amino acids 104-155, 171-198

**FIGURE 313**

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAT  
 GAAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGA  
 ACGAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG  
 AAATAAACAGAGTTAGACCCGCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCC  
 CTCCCCACCCCCAAAAAAGGATGATTGGAATGAAGAACCAGGATTACAAAGAAAAAGTATGTTCAATTT  
 TTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAA  
 AGAACTGGTGTGGTGGTGTTCCTTTCTTTTTGAATTTCCACAAAGAGGAGAGGAAATTAATAATACATCTGC  
 AAAGAAATTTAGAGAAAGAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCA  
 CAGTTGGATTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTTTCTTCATCAACCTCCTTT  
 TTTTAAATTTTTATTCCTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACTGGATTTCCATCT  
 GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAGGACCAACACCAGATAAATTATGAATC  
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAACAGGGCCCTATTTGACCCCT  
 GCTTGTGGTGCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCGGGCTCAGACCTGCCCTTCTGTGT  
 GCTCCTGCAGCAACCAGTTAGCAAGGTGATTTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC  
 ACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAG  
 GCACTTGGAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTCAATGGTCTGGCGA  
 ACCTCAACACTCTGGAACCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAA  
 CTGAAGGAGCTCTGGTTGCGAAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAACAGAATTCCTTCTTT  
 GCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTTATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAAC  
 TGAGGTATTTGAACCTTGCCATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAG  
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAAC  
 GTGGATGATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCA  
 ACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT  
 TTACATCACAACCCTTGGAACGTAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTC  
 GAACACAGCTTGTTGTGCCCCGGTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGA  
 ATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACCTGAAGGCATGGCAGCT  
 GAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCATGACACA  
 TGGGGCGTACAAAGTGCGGATAGCTGTGCTCAGTGATGGTACGTAAATTTACAAATGTAACGTGTGCAAGATA  
 CAGGCATGTACACATGTATGGTGAGTAATTCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCA  
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG  
 GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCACAC  
 CACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCACTGACTGATATAAACAGTGGGATCCCAGGAATT  
 GATGAGGTCATGAAGACTACCAAAATCATCATTTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT  
 GGTCAATTTCTACAAGATGAGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTA  
 TTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTATCGAGCATGAG  
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATTCATACAA  
 CAGTTCAGTGCATGAACGTTATTGATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATCTAAACA  
 TTTACAGAGTTACAAAAACAACAATCAAAAAAAGACAGTTTATTAAAAATGACACAAATGACTGGGCTAA  
 ATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAAGAAAGAAATTTATTTATTAATAAATCTATTG  
 TGATCTAAAGCAGACAAAAA

**FIGURE 314**

MLNKMTLHPQQIMIGPRFNRAFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN  
TTASATLNVTAATTTTFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNTTSLTPQ  
STRSTKFTFTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

**Signal sequence:**

amino acids 1-44

**Transmembrane domain:**

amino acids 523-543

**N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,  
434-438, 442-446, 488-492, 606-610

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

**Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

**N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

**FIGURE 315**

CGCCGCGGAGGCCCATCTGCCCCCAGGGGACAGGGGCGCGGGGCGGGCTCCCGCCCGGCCACAT  
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCCAGCTCGCCCGAGGTCCGTTCGGA  
GGCGCCCGGCCGCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCGCGTCCGGGGATC  
GGG**ATG**TCCCTCCTCCTTCTCCTCTTGCTAGTTTCTACTATGTTGGAACCTTGGGGACTCA  
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC  
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGACAGATTGAACCTCTGAAGC  
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTACAGGGCGCTACGTGTGGAGCCAT  
GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT  
ACTGGCAGCGAATCCGAGAGAAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAATCTAGGATT  
GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA  
CCAGTGACACAGCAGGCAACGAAGCTGGGAAGGAAAAGCTGTGTGGTGCGAGTAACTGTACAGT  
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
ATTTTCCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT  
CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACTCGCTCCACAGCAAAT  
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC  
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG  
CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA  
ACGGTCT**TGA**ATTACAATGGACTTGACTCCCACGCTTTTCCTAGGAGTCAGGGTCTTTGGACTC  
TTCTCGTCAATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTTTCTTATACAATACCAAACAAGCAA  
AGGATGTAAGCTGATTTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
AGGTGAATATACCTAAAACTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTACAAAT  
TTCAAGAGGAAATGGGATGCTGTTTGTAATTTTCTATGCATTTCTGCAAACCTTATTGGATT  
ATTAGTTATTTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
TGAGCTAACCCTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
TTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCAAAATAAC  
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT  
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCTCAAAT  
CAGATGCCTCTAAGGACTTTCTTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT  
TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
CCCAACATACCATTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG  
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

316/330

## **FIGURE 316**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251

Y03280"266T4660



**FIGURE 317**

CGCGAGGCGCGGGGAGCCTGGGACCAGGAGCGAGAGCCGCCTACCTGCAGCCGCCGCCACGGGCACGGCAGCCCA  
CC**ATG**CGCCTCCTGCTGTGCTTCGTGCTCCTGTGCGGAGTAGTGGATTTGCCAGAAAGTTTGAGTATCACTACT  
CCTGAAGAGATGATTGAAAAAGCCAAAGGGGAAACTGCCTATCTGCCATGCAAATTTACGCTTAGTCCCGAAGA  
CCAGGGACCGCTGGACATCGAGTGGCTGATATCACCAGCTGATAATCAGAAGGTGGATCAAGTGATTATTTTAT  
ATTCTGGAGACAAAATTTATGATGACTACTATCCAGATCTGAAAGGCCGAGTACATTTTACGAGTAATGATCTC  
AAATCTGGTGATGCATCAATAAATGTAACGAATTTACAAGTGTGAGATATTGGCACATATCAGTGCAAAGTGAA  
AAAAGCTCCTGGTGTTGCAAATAAGAAGATTCATCTGGTAGTTCTTGTTAAGCCTTCAGGTGCGAGATGTTACG  
TTGATGGATCTGAAGAAATTGGAAGTGACTTTAAGATAAAATGTGAACCAAAGAAGGTTCACTTCCATTACAG  
TATGAGTGGCAAAAATTTGCTGACTCACAGAAAATGCCCACTTCATGGTTAGCAGAAATGACTTCATCTGTTAT  
ATCTGTAAAAAATGCCTCTTCTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAAACAGAGTGGGCTCTGATC  
AGTGCTGTTTGGCTCTAAACGTTGTCCCTCCTTCAAATAAAGCTGGACTAATTGCAGGAGCCATTATAGGAACT  
TTGCTTGCTCTAGCGCTCATTGGTCTTATCATCTTTTGCTGTGCTGTAAGGCGCAGAGAAGAAAAATATGAAAA  
GGAAGTTCATCACGATATCAGGGAAGATGTGCCACCTCCAAAGAGCCGTACGTCCACTGCCAGAAGCTACATCG  
GCAGTAATCATTCATCCCTGGGGTCCATGTCTCCTTCCAACATGGAAGGATATTCCAAGACTCAGTATAACCAA  
GTACCAAGTGAAGACTTTGAACGCACTCCTCAGAGTCCGACTCTCCACCTGCTAAGTTCAGTACCCCTTACAA  
GACTGATGGAATTACAGTTGTAT**TAA**AATATGGACTACTGAAGAATCTGAAGTATTGTATTATTTGACTTTATTTT  
AGGCCTCTAGTAAAGACTTAAATGTTTTTAAAAAAGCACAAGGCACAGAGATTAGAGCAGCTGTAAGAACAC  
ATCTACTTTATGCAATGGCATTAGACATGTAAGTCAGATGTCATGTCAAAATTAGTACGAGCCAAATCTTTGT  
TAAAAAACCTATGTATAGTGACACTGATAGTTAAAAGATGTTTTATTATATTTTCAATAACTACCACTAACAA  
ATTTTAACTTTTCATATGCATATTCTGATATGTGGTCTTTTAGGAAAAGTATGGTTAATAGTTGATTTTCAA  
AGGAAATTTTAAATTTCTACGTTCTGTTAATGTTTTTGCTATTTAGTTAAATACATTGAAGGGAATACCCG  
TTCTTTTCCCCTTTTATGCACACAACAGAAAACACGCGTTGTCATGCTCAAACATATTTTATTTGCAACTACA  
TGATTTACACAATTTCTCTTAAACAACGACATAAAATAGATTTCTTGTATATAAATAACTTACATACGCTCCA  
TAAAGTAAATTTCTCAAAGGTGCTAGAACAAATCGTCCACTTCTACAGTGTCTCGTATCCAACAGAGTTGATGC  
ACAATATATAAAATACTCAAGTCCAATATTAAAAAAGTTAGGCACTTGACTAACTTTAATAAAATTTCTCAAAC  
TATCAATATCTAAAGTGCAATATTTTTTAAAGAAAGATTATTCTCAATAACTTCTATAAAAAATAAGTTTGATGG  
TTTGGCCCATCTAACTTCACTACTATTAGTAAGAAGTTTAACTTTTAAATGTGTAGTAAGGTTTATTCTACCTT  
TTTCTCAACATGACACCAACACAATCAAAAACGAAGTTAGTGAGGTGCTAACATGTGAGGATTAATCCAGTGAT  
TCCGGTCACAATGCATTTCCAGGAGGAGGTACCCATGTCACCTGGAATTGGGCGATATGGTTTATTTTCTTCCC  
TGATTTGGATAACCAAATGGAACAGGAGGAGGATAGTGATTCTGATGGCCATTCCCTCGATACATTCTCGGCTT  
TTTTCTGGGCAAAGGGTGCCACATTGGAAGAGGTGGAAATATAAGTTCTGAAATCTGTAGGGAAGAGAACACAT  
TAAGTTAATTTCAAAGGAAAAAATCATCATCTATGTTCCAGATTTCTCATTAAGACAAAGTTACCCACAACACT  
GAGATCACATCTAAGTGACACTCCTATTGTGAGGTCTAAATACATTAAAAACCTCATGTGTAATAGGCGTATAA  
TGATAACAGGTGACCAATGTTTTCTGAATGCATAAAGAAATGAATAAACTCAAACACAGTACTTCTTAAACAA  
CTTCAACCAAAAAAGACCAAAACATGGAACGAATGGAAGCTTGTAAAGGACATGCTTGTTTTAGTCCAGTGGTTT  
CCACAGCTGGCTAAGCCAGGAGTCACTTGGAGGCTTTTAAATACAAAACATTGGAGCTGGAGGCCATTATCCTT  
AGCAAACATAATGCAGAAACAGAAAATCAACTACCGCATGTTCTCACTTATAAGTGGGAGGTAATGATAAGAACT  
TATGAACACAAAGAAGGAACAATAGACATTGGAGTCTATTTGAGAGGGGAGGGTGGGAGAAGGAAAAGGAGCA  
GAAAAGATAACTATTGAGTACTGCCTTCACACCTGGGTGATGAAATAATATGTACAACAATCCCTGTGACACA  
TGTTTACCTATGGAACAAACCTTCATGTGTATCCCTAAACCTAAAAATAAAAGTTAAAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 318**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLCFVLLCGVVDFAFARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPA  
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK  
APGVANKKIHLVVLVKPSGARCIVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT  
SWLAEMTSSVISVKNASSEYSGTYSTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL  
ALALIGLIIFFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM  
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

**Signal sequence.**

amino acids 1-19

**Transmembrane domain:**

amino acids 236-257

**N-glycosylation sites.**

amino acids 106-110, 201-205, 298-302

**Tyrosine kinase phosphorylation sites.**

amino acids 31-39, 78-85, 262-270

**N-myristoylation sites.**

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,  
245-251, 296-302

**Myelin P0 protein.**

amino acids 96-125

**FIGURE 319**

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA  
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC  
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGC  
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG  
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC  
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTG  
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT  
 GAAGGGGGTGTTCCTCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG  
 CTCAGGATAACATCACGAGTCCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGAT  
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAAGTGTTCAAAAA  
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC  
 TTGTTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC  
 AGTGCACACAGGCGGTTTTCTGCTATTCGGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC  
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATCTACAAGC  
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTTCA  
 AACAGTCTCCCTTCCTATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATT  
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG  
 GTGCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTT  
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG  
 CAGCAGAATATTGTGCCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG  
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT  
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACTGAACTTCAGAGCATGAAAATCACACT  
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGGTAAGGTGCATCTGTTTGAAAAG  
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT  
 TCCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTT  
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC  
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA  
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 320**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPLLATASQMOMVVLPCLGFTLLLWSQVSGAQGQEFHFGPCQVK  
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH  
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL  
TKALGEVDILLTWMQKFYKL

**Signal sequence:**

amino acids 1-42

**N-glycosylation sites.**

amino acids 85-89, 99-103, 126-130

**FIGURE 321**

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGC**ATG**AAGTTACAGTGTGTTTCCCTTTGGCTC  
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC  
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG  
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA  
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTTCAAGGATCA  
TCAGGAGCCAAACCCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA  
TGCAGAAAACCTCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC  
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA  
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT  
CAGCT**TGA**TGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCCTGTGCGGTTTACT  
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC  
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAAATAGGCAAAAAGTCTACTGTGGTAT  
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT  
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT  
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATTCCATATTTTACCTATGA

**FIGURE 322**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHDNYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA
```

**Signal sequence:**

amino acids 1-18

**N-glycosylation sites.**

amino acids 56-60, 135-139

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 102-106

**N-myristoylation site.**

amino acids 24-30

**Actinin-type actin-binding domain signature 1.**

amino acids 159-169

**FIGURE 323**

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG  
AACGCGGCTACAATTAATACATAACCTTATGTATCATAACATACGATTTAGGTGACACTAT  
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTC  
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCCGCCT  
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA  
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC  
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC  
CATCTACAGTGGCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA  
TGAGCAGAAGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTTTCGAC  
CCGGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCC  
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC  
CACCCCCGTACTCCCAGTTCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTTCAACACC  
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGT  
GCTGAAGCCCCGGGCCCCGGATGACCCCGGCCCCGGCCTCCTGTTTACAGGAGCTCCCGAGCG  
CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCGAGTGAAC  
ACGCACGCTGGGGGAACGGGCCCCGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTTCG  
CTGG

**FIGURE 324**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVD  
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLENGY  
DVIHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSE  
RDPLNLVKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA  
KFI

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 175-179

**N-myristoylation site.**

amino acids 33-39, 100-106, 225-231, 229-235

**HBGF/FGF family proteins**

amino acids 73-124



**FIGURE 325**

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**  
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCCTTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG  
 GAGCTCTGCAGGCCCCAGCACCCGCAGAGCAGACACTGCGATGACAACGGACGACACAGAAG  
 TGCCCGCTATGACTCTAGCACCGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG  
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA  
 GAGAATTTCCCCTGCAAGAGAGACCAGGAGTTTCACAAAACATCTCCCAACTTCATGGTGC  
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC  
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTTCACCCGA  
 TGACAGCTCTGAAGAGGCCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA  
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC  
 ACCCCGTACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCC  
 GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCCGTCT  
 GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCACAAACATCGAG  
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACAACCTTCCAGCATCCCTGGGGCCTCAGA  
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCTCGTCCACCTCCGATCCACCAGCTCTGC  
 CTGACTCCACTGAAGCAAAACCACACATCACTGAGGTACAGCCTCTGCCGAGACCCCTGTCC  
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCCACTCCCCACTAA  
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGGAGCTCTGGTCA  
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC  
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTGAGCAGTGGGCAAAACAACCTTC  
 CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCCTCGGAAGCCGCCCTCAAGAACTTCACCC  
 CTTCAGAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACCAGCAGGGACCCT  
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA  
 GATCACAACCTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCCACGACTGCCCGGAC  
 GAGGCCGACCACAGACG**TGAG**TGCAGGTGAAAATGGAGGTTTCCTCCTCCTGCGGCTGAGTG  
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC  
 CGGGAACCTCCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTCAGGAGAGGCTA  
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG  
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG  
 AAGGGCAGCATGTCCAAGCCCCTAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC  
 CGGAGTGTATGTATGGGGAGGGGCTTCACCTGTTCCAGAGGTGTCCTTGGACTCACCTTGG  
 CACATGTTCTGTGTTTCAGTAAAGAGAGACCTGATCACCCATCTGTGTGCTTCCATCCTGCA  
 TTAAATTCACCTCAGTGTGGCCCCAAAAAAA

**FIGURE 326**

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL  
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSNFMVLIATSVETSAASGSPEGAGM  
 TTVQTITGSDPEEAI FDTLCTDDSSSEEAKTLTMDILT LAHTSTEAKGLSSESSASSDGPHPV  
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTL LAEALVTVTNI  
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL  
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLSGALVTVSRNPLEETSALSVETPSY  
 VKVSGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTSRD  
 PLPSVPPTTTNSSRGTNSTLAKITTS AKTTMKPQQPRPRLPGRGRPQT

**N-glycosylation sites:**

amino acids 252-256, 445-449, 451-455

**cAMP-and cGMP-dependent protein kinase phosphorylation site.**

amino acids 84-90

**Casein kinase II phosphorylation sites.**

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,  
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,  
 404-408, 414-418, 431-435

**N-myristoylation sites.**

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-  
 320, 349-355, 386-392, 397-403, 449-455

**ATP/GTP-binding site motif A (P-loop).**

amino acids 385-393

0904199-0330  
 10220 254455

**FIGURE 327**

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCCGCGCGGATTCGCCGGTCTTCCCGCGG  
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA  
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAATAAGACCAGAGGGAGGATTAT  
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATATGTTCTTCGGGGGAGAAGGGAG  
 CTTGACTTACACTTTTGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT  
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC  
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTTCAAC  
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA  
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA  
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAAGCAGTCACTCCCC  
 TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT  
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA  
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA  
 TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCA  
 CATAACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC  
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
 AGCCTCCCACGACCCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG  
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA  
 AACCATAACGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCTA  
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT  
 AGGGAGGCCAGTCCAGGCAGTTCTTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCC  
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGTTGGTATAGGCC  
 TCGTCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT  
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT  
 TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG  
 TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTCCTTTTTTTTTTTGGAGACAGAGTCTT  
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC  
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
 CCACACCTGGGTGATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTG  
 GTCTCAAACCTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG  
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTTGGTTTTTGGAGAAGGAATGAAGTG  
 GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAAGCTCT  
 ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA  
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCCAGATAAAATCAAC  
 TGTTTATATCAATTTCTAATGGATTTGCTTTTCTTTTTATATGGATTCTTTTAAACTTATT  
 CCAGATGTAGTTCTTCCAATTAAATATTTGAATAAATCTTTTGTTACTCAA

**FIGURE 328**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED  
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP  
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF  
KMDEASAQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL  
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP  
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV  
PENQYGLPFEEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI

**Signal sequence.**

amino acids 1-25

**Transmembrane domain.**

amino acids 384-405

**N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

**Tyrosine kinase phosphorylation site.**

amino acids 50-57

**N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321

**FIGURE 329**

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT  
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT  
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA  
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG  
 TCTTTACTGATCTCTCTGTTCTGTTTCCAGGACCCTGCTGTCTTCCCTCCCCCTTCTCCAC  
 CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC  
 CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCCGGCCCCCATGCAGC  
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCCTGGTGCTGCTGAGCCTTCTGTCAGC  
 CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC  
 CCTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA  
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT  
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGATGTTCCA  
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
 GAGACTGGGACATCCCTGATAGGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA  
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC  
 CTCATGCCCAGTGTGCGACCCTGCCTTCCCTCCACTCCAGACCCACCTTGTCTTCCCTCCC  
 TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT  
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTTCAGGAAGCCT  
 GTGAAAAACGTGATTCCCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
 GACTCTGAATTCTAACAATGCCAGTGACTGTGCACTTGAGTTTGAAGGGCCAGTGGGCCTG  
 ATGAACGCTCACACCCCTTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC  
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG  
 TCCAGGCCTTGGTCAAGTCAAGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG  
 TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCTTTGGAAAAAATGATGAAGA  
 AAACCTTGGCTCCTTCCCTTGTCTGAAAGGGTTACTTGCTATGGGTCTGGTGGCTAGAGA  
 GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA  
 GCACAATACTATTTTTTTTTCTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT  
 GCTGCCCAGGCTGGAGTGCAGTGGCAGATCTGCAAACCTCCGCCTCCTGGGTTCAAGTGATT  
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT  
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC  
 CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG  
 TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCAGTATGCAAACTTGGAAG  
 ATGGAGGAGAAAAAGAAAAGGAAGAAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT  
 TATTTTCGTTTTGTGTACTTCCCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTTCTT  
 TTTACAGAGCAATTATCTTGTATATAACAATTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
 ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTTTATAAATAAAATGTTTCATCA  
 GCTGCATAAAAAAAAAAAAAA

**FIGURE 330**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPTEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAE EEGQETMKGRVSIRD SRQELSLIVTLWNLTQLQDAGEYWCGVEKRGPD ELLISLFV  
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD  
VISMPPPLHTSEEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128